# Ҥ. .ſENT COOPERATION TREAⅠ́

## PCT

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**Applicant**

MORELL, Matthew et al

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|---|---|
| Facsimile No.: (41-22) 740.14.35 | Telephone No.: (41-22) 338.83.38 |

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**(54) Title:** NOVEL GENES ENCODING WHEAT STARCH SYNTHASES AND USES THEREFOR

**(57) Abstract**

The present invention provides isolated nucleic acid molecules encoding wheat starch synthases, and probes and primers derived therefrom, which are useful in the modificaiton of plant starch content and/or composition, and for screening plant lines to determine the presence of natural and/or induced mutations in starch synthase genes which affect starch content and/or composition. More particularly, the isolated nucleic acid molecules of the present invention further provide for the screening–assisted breeding of plants having desirable starch content and/or composition, in addition to providing for the direct genetic manipulation of plant starch content and/or composition.

**FIGURE 1**

| FIGURE 2A |
|---|
| FIGURE 2B |
| FIGURE 2C |
| FIGURE 2D |
| FIGURE 2E |
| FIGURE 2F |
| FIGURE 2G |
| FIGURE 2H |
| FIGURE 2I |
| FIGURE 2J |
| FIGURE 2K |
| FIGURE 2L |
| FIGURE 2M |
| FIGURE 2N |
| FIGURE 2O |

# FIGURE 2

```
1                                                          50
wSSIIB   ATTTCCTCGG CCTGACCCCG TGCGTTTACC CCACACAGAG CACACTCCAG
wSSIID   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
wSSIIA   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

51                                                        100
wSSIIB   TCCAGTCCAG CCCACTGCCG CGCTACTCCC CACTCCCACT GCCACCACCT
wSSIID   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
wSSIIA   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~GCT GCCACCACCT

101                                                       150
wSSIIB   CCGCcTGCGC CGCGGCTCTGG GCGGACCAAC CCGCGGCATCG TATCACGATC
wSSIID   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
wSSIIA   CCGCCTGCGC CGCGCTCTGG GCGGAGGACC AACCCGCGCA TCGTACCATC

151                                                       200
wSSIIB   ACCCACCCCG ATCCCGGCCG CCGCCATGTC GTCGGGCGGTC GCGTCCGCCG
wSSIID   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
wSSIIA   GCCGCCCCG ATCCCGGCCG CCGCCATGTC GTCGGGCGGTC GCGTCCGCCG
```

FIGURE 2A

```
201                                                  250
wSSIIB  CGTCCTTCCT CGCGCTCGCG TCCGCCTCCC CCGGGAGATC ACGGAGGAGG
wSSIID  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
wSSIIA  CGTCCTTCCT CGCGCTCGCC TCCGCCTCCC CCGGGAGATC ACGCAGGCGG

251                                                  300
wSSIIB  ACGAGGGTGA GCGCGTCGCC ACCCCACACC GGGGCTGGCA GGTTGCACTG
wSSIID  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
wSSIIA  GCGAGGGTGA GCGGCCGCC ACCCCACGCC GGGGCCGGCA GGCTGCACTG

301                                                  350
wSSIIB  GCCGCCGTCG CCGCCCGCAGC GCACGGCTCG CGACGGAGCG GTGGCCGCGC
wSSIID  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
wSSIIA  GCCGCCGTGG CCGCCGCAGC GCACGGCTCG CGACGGAGGT GTGGCCGCGC

351                                                  400
wSSIIB  GCGCCGCCGG GAAGAAGGAC GCGGGGGAT.. .CGACGACGC CGCGCCCGCG
wSSIID  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
wSSIIA  GCGCCGCCGG GAAGAAGGAC GCGAGGGTCG ACGACGACGC CGCGTCCGCG
```

**FIGURE 2B**

```
                                                              450
401
wSSIIB  AGGCAGCCCC  GCGCACTCCG  CGGTGGCGCC  GCCACCAAGG  TTGCGGAGCG
wSSIID  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~
wSSIIA  AGGCAGCCCC  GCGCACGCCC  CGGTGGCGCC  GCCACCAAGG  TCGCGGAGCG

                                                              500
451
wSSIIB  GAGGGATCCC  GTCAAGACGC  TCGATCGCGA  CGCCGCGGAA  GGTGGCGCGC
wSSIID  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~
wSSIIA  GAGGGATCCC  GTCAAGACGC  TCGATCGCGA  CGCCGCGGAA  GGTGGCGCGC

                                                              550
501
wSSIIB  CGTCCCCGCC  GGCACCGAGG  CAGGAGGACG  CCCGTCTGCC  GAGCATGAAC
wSSIID  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~
wSSIIA  CGGCACCGCC  GGCACCGAGG  CAGGACGCCG  CCCGTCCaCC  GAGTATGAAC

                                                              600
551
wSSIIB  GGCATGCCGG  TGAACGGTGA  AAACAAATCT  ACCGGGCGGCG  GCGGCGGAC
wSSIID  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~
wSSIIA  GGCACGCCGG  TGAACGGTGA  GAACAAATCT  ACCGGGCGGCG  GCGGCGGAC
```

FIGURE 2C

```
601                                                              650
wSSIIB  TAAAGACAGC GGGCTGCCCG CACCCGCACG CGGCGCCCAG CCGTCGAGCC
wSSIID  ~~~~~~~~~~ ?          ?          ?          ?
wSSIIA  CAAAGACAGC GGGCTgcCCG CACCCGcACG CGCGCCCCAT CCGTCGAcCC

651                                                              700
wSSIIB  AGAACAGAGT ACCGGTGAAT GGTGAAAACA AAGCTAACGT CGCCTCGCCG
wSSIID  ~~~~~~~~~~ ?          ?          ?          ?
wSSIIA  AgAACAgAGT ACCAGTGAAC GGTGAAAACA AAGCTAACGT CGCCTCGCCG

701                                                              750
wSSIIB  CCGACGAGCA TAGCCGAGGT CGCGGCTCCG GATCCCGCAG CTACCATTTC
wSSIID  ~~~~~~~~~~ ?          ?          ?          ?
wSSIIA  CCGACGAGCA TAGCCGAGGT CGTGGCTCCG GATTCCGCAG CTACCATTTC

751                                                              800
wSSIIB  CATCAGTGAC AAGGCGCCAG AGTCCGTTGT CCCAGCCGAG AAGGcgccgc
wSSIID  ~~~~~~~~~~ ?          ?          ~CCAGCTGAG AAGACGCCGC
wSSIIA  CATCAGTGAC AAGGCGCCGG AGTCCGTTGT CCCAGCCGAG AAGCCGCCGC
```

**FIGURE 2D**

```
        801                                              850
wSSIIB  CGtCgtcCgg CtcAAAaTtc gtgCcCtcgg cttctgCtcc cggGtctGAC
wSSIID  CGTCGTCCGG CTCAAATTTC GAGTCCTCGG CCTCTGCTCC CGGGTCTGGAC
wSSIIA  CGTCGTCCGG CTCAAATTTC GTGgTCTCGG CTTCTGCTCC CAGGCTGGGAC

        851                                              900
wSSIIB  actgtCaGCG acGtGGaact TgaActGAAg aAGGGtgCgg tCattgTcaA
wSSIID  ACTGTCAGCG ACGTGGAACA AGAACTGAAG AAGGGTGCGG TCGTTGTCGA
wSSIIA  ATTGACAGCG ATGTTGAACC TGAACTGAAG AAGGGTGCGG TCATCGTCGA

        901                                              950
wSSIIB  aGAAgcTcCa aaCcCaAaGG CTCTTTCGCC GCCCGCAGCA CCCGCTGTAC
wSSIID  AGAAGCTCCA AAGCCAAAGG CTCTTTCGCC GCCtGCAGCC CCCGCTGTAC
wSSIIA  AGAAGCTCCA AACCCAAAGG CTCTTTCGCC GCCTGCAGCC CCCGCTGTAC

        951                                              1000
wSSIIB  AACAAGACCT TTGGGACTTC AAGAAATACA TTGGTTTCGA GGAGCCCGTG
wSSIID  AAgAAGACCT TTGGGAtTTC AAGAAATACA TTGGTTTCGA GGAGCCCGTG
wSSIIA  AAGAAGACCT TTGGGACTTC AAGAAATACA TTGGCTTCGA GGAGCCCGTG
```

**FIGURE 2E**

```
                                                                                                1050
1001
wSSIIB   GAGGCCAAGG   ATGATGGCCG   GGCTGTTGCA   GATGATGCGG   GCTCCTTCGA
wSSIID   GAGGCCAAGG   ATGATGGCCG   GGCTGTCGCA   GATGATGCGG   GCTCCTTtGA
wSSIIA   GAGGCCAAGG   ATGATGGCTG   GGCTGTTGCA   GATGATGCGG   GCTCCTTTGA

                                                                                                1100
1051
wSSIIB   ACACCACCAG   AATCACGATT   CCGGGCCTTT   GGCAGGGGAG   AACGTCATGA
wSSIID   ACACCACCAG   AATCACGACT   CCGGaCCTTT   GGCAGGGGAG   AAtGTCATGA
wSSIIA   ACATCACCAG   AACCATGATT   CCGGACCTTT   GGCAGGGGAG   AACGTCATGA

                                                                                                1150
1101
wSSIIB   ACGTGGTCGT   CGTGGCTGCT   GAATGTTCTC   CCTGGTGCAA   AACAGGTGGT
wSSIID   ACGTGGTCGT   CGTGGCTGCT   GAgTGTTCTC   CCTGGTGCAA   AACAGGTGGT
wSSIIA   ACGTGGTCGT   CGTGGCTGCT   GAATGTTCTC   CCTGGTGCAA   AACAGGTGGT

                                                                                                1200
1151
wSSIIB   CTTGGAGATG   TTGCCGGTGC   TTTGCCCAAG   GCTTTGGGCGA   AGAGAGGACA
wSSIID   CTgGGAGATG   TTGCgGGTGC   TcTGCCCAAG   GCTTTGGCaA    AGAGAGGACA
wSSIIA   CTTGGAGATG   TTGCCGGTGC   TTTGCCCAAG   GCTTTGGGCGA   AGAGAGGACA
```

**FIGURE 2F**

```
1201                                                    1250
wSSIIB  TCGTGTTATG GTTGTGGTAC CAAGGTATGG GGACTATGAG GAAGCCTACG
wSSIID  TCGTGTTATG GTTGTGGTAC CAAGGTATGG GGACTATGAa GAACCTACGg
wSSIIA  TCGTGTTATG GTTGTGGTAC CAAGGTATGG GGACTATGAG GAAGCCTACG

1251                                                    1300
wSSIIB  ATGTCGGAGT CCGAAAATAC TACAAGGCTG CTGGACAGGA TATGGAAGTG
wSSIID  ATGTCGGAGT CCGAAAATAC TACAAGGCTG CTGGACAGGA TATGGAAGTG
wSSIIA  ATGTCGGAGT CCGAAAATAC TACAAGGCTG CTGGACAGGA TATGGAAGTG

1301                                                    1350
wSSIIB  AATTATTTCC ATGCTTATAT CGATGGGAGTT GATTTGTGT TCATTGACGC
wSSIID  AATTATTTCC ATGCTTaTAT CGATGGGAGTT GATTTGTGT TCATTGACGC
wSSIIA  AATTATTTCC ATGCTTATAT CGATGGGAGTT GATTTGTGT TCATTGACGC

1351                                                    1400
wSSIIB  TCCTCTCTTC CGACACCGCC AGGAAGACAT TTATGGGGGC AGCAGACAGG
wSSIID  TCCTCTCTTC CGACACCGAG AGGAAGACAT TTATGGGGGC AGCAGACAGG
wSSIIA  TCCTCTCTTC CGACACCGCC AGGAAGACAT TTATGGGGGC AGCAGACAGG
```

FIGURE 2G

```
              1401
     wSSIIB   AAATTATGAA   GCGCATGATT   TTGTTCTGCA   AGGCCGCTGT
     wSSIID   AAATTATGAA   GCGCATGATT   TTGTTCTGCA   AGGCCGCTGT
     wSSIIA   AAATTATGAA   GCGCATGATT   TTGTTCTGCA   AGGCCGCTGT

                                                                  1450
     wSSIIB   CGAGGTTCCA
     wSSIID   TGAGGTTCCA
     wSSIIA   CGAGGTTCCT

              1451
     wSSIIB   TGGCACGTTC   CATGCGGCGG   TGTCCCTTAT   GGGGATGGAA
     wSSIID   TGGCACGTTC   CATGCGGCGG   TGTCCCTTAT   GGGGATGGAA
     wSSIIA   TGGCACGTTC   CATGCGGCGG   TGTCCCTTAT   GGGGATGGAA

                                                                  1500
     wSSIIB   ATCTGGTGTT
     wSSIID   ATCTGGTGTT
     wSSIIA   ATCTGGTGTT

              1501
     wSSIIB   TATTGCAAAT   GATTGGCACA   CGGCACTCCT   GCCTGTCTAT
     wSSIID   TATTGCAAAT   GATTGGCACA   CGGCACTCCT   GCCTGTCTAT
     wSSIIA   TATTGCAAAT   GATTGGCACA   CGGCACTCCT   GCCTGTCTAT

                                                                  1550
     wSSIIB   CTGAAAGCAT
     wSSIID   CTGAAAGCAT
     wSSIIA   CTGAAAGCAT

              1551
     wSSIIB   ATTACAGGGA   CCATGGTTTG   ATGCAGTACA   CTCGGTCCAT
     wSSIID   ATTACAGGGA   CCATGGTTTG   ATGCAGTACA   CTCGGTCCAT
     wSSIIA   ATTACAGGGA   CCATGGTTTG   ATGCAGTACA   CTCGGTCCAT

                                                                  1600
     wSSIIB   TATGGTGATA
     wSSIID   TATGGTGATA
     wSSIIA   TATGGTGATA
```

# FIGURE 2H

```
      1601                                              1650
wSSIIB  CATAACATCG CTCACCAGGG CCGTGGCCCA GTAGATGAGT TCCCGTTCAC
wSSIID  CATAACATCG CTCACCAGGG CCGTGGCCCT GTAGATGAAT TCCCGTTCAC
wSSIIA  CATAACATCG CGCACCAGGG CCGTGGCCCA GTAGATGAAT TCCCGTTCAC

      1651                                              1700
wSSIIB  CGAGTTGCCT GAGCACTACC TGGAACACTT CAGACTGTAC GACCCCGTGG
wSSIID  CGAGTTGCCT GAGCACTACC TGGAACACTT CAGACTGTAC GACCCCGTGG
wSSIIA  CGAGTTGCCT GAGCACTACC TGGAACACTT CAGACTGTAC GACCCCGTGG

      1701                                              1750
wSSIIB  GTGGTGAACA CGCCAACTAC TTCGCCGCCG GCCTGAAGAT GGCGGACCAG
wSSIID  GTGGTGAACA CGCCAACTAC TTCGCCGCCG GCCTGAAGAT GGCGGACCAG
wSSIIA  GTGGTGAGCA CGCCAACTAC TTCGCCGCCG GCCTgAAGAT GgCGGACCAG

      1751                                              1800
wSSIIB  GTTGTCGTCG TGAGCCCGGG GTACCTGTGG GAGCTGAAGA CGGTGGGAGGG
wSSIID  GTTGTCGTGG TGAGCCCCGG GTACCTGTGG GAGCTGAAGA CGGTGGGAGGG
wSSIIA  GTTGTCGTGG TGAGCCCCGG GTACCTGTGG gAGCTCAAGA CGGTGGGAGGG
```

FIGURE 2I

```
                1801                                              1850
        wSSIIB  CGGCTGGGGG CTTCACGACA TCATACGGCA GAACGACTGG AAGACCCGCG
        wSSIID  CGGCTGGGGG CTTCACGACA TCATACGGCA GAACGACTGG AAGACCCGCG
        wSSIIA  CGGCTGGGGG CTTCACGACA TCATACGGCA GAACGACTGG AAGACCCGCG

                1851                                              1900
        wSSIIB  GCATCGTGAA CGGCATCGAC AACATGGAGT GGAACCCCGA GGTGGACGTC
        wSSIID  GCATCGTCAA CGGCATCGAC AACATGGAGT GGAACCCCGA GGTGGACGCC
        wSSIIA  GCATCGTCAA CGGCATCGAC AACATGGAGT GGAACCCCGA GGTGGACGTC

                1901                                              1950
        wSSIIB  CACCTCAAGT CGGACGGCTA CACCAACTTC TCCCTGGGGA CGCTGGACTC
        wSSIID  CACCTCAAGT CGGACGGCTA CACCAACTTC TCCCTGAGGA CGCTGGACTC
        wSSIIA  CACCTCAAGT CGGACGGCTA CACCAACTTC TCCCTGGGGA CGCTGGACTC

                1951                                              2000
        wSSIIB  CGGCAAGCGG CAGTGCAAGG AGGCCCTGCA GCGGGAGCTG GGCCTGCAGG
        wSSIID  CGGCAAGCGG CAGTGCAAGG AGGCCCTGCA GCGCGAGCTG GGCCTGCAGG
        wSSIIA  CGGCAAGCGG CAGTGCAAGG AGGCCCTGCA GCGCGAGCTG GGCCTGCAGG
```

**FIGURE 2J**

```
                2001                                              2050
wSSIIB   TCCGGGGCGA  CGTGCCGCTG  CTCGGCTTCA  TCGGGCGCCT  GGACGGGCAG
wSSIID   TCCGGCGCGA  CGTGCCGCTG  CTCGGCTTCA  TCGGGCGCCT  GGACGGGCAG
wSSIIA   TCCGCGCCGA  CGTGCCGCTG  CTCGGCTTCA  TCGGCCGCCT  GGACGGGCAG

                2051                                              2100
wSSIIB   AAGGGCGTGG  AGATCATCGC  GGACGCGGATG CCCTGGATCG  TGAGCCAGGA
wSSIID   AAGGGCGTGG  AGATCATCGC  GGACGCCATG  CCCTGGATCG  TGAGCCAGGA
wSSIIA   AAGGGCGTGG  AGATCATCGC  GGACGCCATG  CCCTGGaTCG  TGAGCCAGgA

                2101                                              2150
wSSIIB   CGTGCAGCTG  GTCATGCTGG  GCACCGGGCG  CCACGACCTG  GAGGGCATGC
wSSIID   CGTGCAGCTG  GTGATGCTGG  GCACCGGGCG  CCACGACCTG  GAGAGCATGC
wSSIIA   CGTGCAGCTG  GTCATGCTGG  GCACCGGCCG  CCACGACCTG  gAGAGCATGc

                2151                                              2200
wSSIIB   TGCGGCACTT  CGAGCGGGAG  CACCACGACA  AGGTGCGCGG  GTGGGTGGGG
wSSIID   TGCAGCACTT  CGAGCGGGAG  CACCACGACA  AGGTGCGCGG  GTGGGTGGGG
wSSIIA   TgCGGCACTT  CGAGCGGGAG  CACCACGACA  AGGTGCGCGG  gTGGGTGGGG
```

## FIGURE 2K

```
        2201
wSSIIB  TTCTCCGTGC  GGCTGGCGCA  CCGGATCACG  GCCGGCGCCG
wSSIID  TTCTCCGTGC  GCCTGGCGCA  CCGGATCACG  GCGGGGGCGG
wSSIIA  TTCTCCGTgc  GCcTGGCGCA  CCGGATCACG  GCGGGCGCCG

        2251
wSSIIB  CATGCCCTCC  CGGTTCGAGC  CGTGCGGACT  GAACCAGCTC
wSSIID  CATGCCCTCC  CGGTTCGTGC  CGTGCGGGCT  GAACCAGCTC
wSSIIA  CATGCCCTCC  CGGTTCGAgC  CGTGCGGGTT  GAACCAGCTt

        2301
wSSIIB  CCTACGGCAC  CGTCCCCGTC  GTGCATGCCG  TCGGTGGCCT
wSSIID  CCTACGGCAC  CGTCCCCGTC  GTGCACGCCG  TCGGCGGCCT
wSSIIA  CCTACGGCAC  CGTCCCCGTC  GTGCACGCCG  TCGGGCGGGT

        2351
wSSIIB  GTGCCGCCGT  TCGACCCCTT  CAACCACTCC  GGGCTCGGGT
wSSIID  GTGCCGCCGT  TCGACCCCTT  CAACCACTCC  GGGCTCGGGT
wSSIIA  GTGCCGCCGT  TCGACCCCTT  CAACCACTCC  GCCTCGGGT
```

```
        2250
ACGCGCTCCT
ACGCGCTCCT
ACGCGCTCCT

        2300
TACGCCATGG
TACGCCATGG
TACGCCATGG

        2350
GAGGGACACC
CAGGGACACC
GAGGGACACC

        2400
GGACGTTCGA
GGACGTTCGA
GGACGTTCGA
```

# FIGURE 2L

```
         2401                                               2450
wSSIIB   CCGGCGAGAG  GCGCAGAAGC  TGATCGAGGC  GCTCGGGCAC  TGCCTCCGCA
wSSIID   CCGCGCCGAG  GCGCACAAGC  TGATCGAGGC  GCTCGGGCAC  TGCCTCCGCA
wSSIIA   CCGCGCCGAG  GCGCACAAGC  TGATCGAGGC  GCTCGGGCAC  TGCCTCCGCA

         2451                                               2500
wSSIIB   CCTACCGGGA  CTACAAGGAG  AGCTGGAGGG  GGCTCCAGGA  GCGCGGCATG
wSSIID   CCTACCGAGA  CTTCAAGGAG  AGCTGGAGGG  CCCTCCAGGA  GCGCGGCATG
wSSIIA   CCTACCGGGA  CTACAAGGAG  AGCTGGAGGG  GCCTCCAGGA  GCGCGGCATG

         2501                                               2550
wSSIIB   TCGCAGGACT  TCAGCTGGGA  GCATGCCGCC  AAGCTCTACG  AGGACGTCCT
wSSIID   TCGCAGGACT  TCAGCTGGGA  GCACGCCGCC  AAGCTCTACG  AGGACGTCCT
wSSIIA   TCGCAGGACT  TCAGCTGGGA  GCATGCCGCC  AAGCTCTACG  AGGACGTCCT

         2551                                               2600
wSSIIB   CGTCAAGGCC  AAGTACCAGT  GGTGAACGCT  AGCTGCTAGC  CGGTCCCAGCC
wSSIID   CGTCAAGGCC  AAGTACCAGT  GGTGAACGCT  AGCTGCTAGC  CGCTCCAGCC
wSSIIA   CCTCAAGGCC  AAGTACCAGT  GGTGAACGCT  AGCTGCTAGC  CGCTCCAGCC
```

**FIGURE 2M**

```
        2601
wSSIIB  CCGCATGCCG. ...TGCATGA CAGGATGGAA TTGCGCATTG CGCACGCAGG
wSSIID  CCGCATGCCG. ...TGCATGA CAGGATGGAA CT..GCATTG CGCACGCAGG
wSSIIA  CCGCATGCGT GCATGcatgA gAGGgTGGAA CTGCGCATTG CGCCCGCAGG
                                                              2650

        2651
wSSIIB  AAGGTGCCAT ......... .GGAGCGCCG GCATCCGCGA AGTACAGTGA
wSSIID  AAAGTGCCAT ......... .GGAGCGCCG GCATCCGCGA AGTACAGTGA
wSSIIA  AAcGTGCCAT ccttctcgat gGGAGCGCCG GCATCCGCGA gGTgCAGTGA
                                                              2700

        2701
wSSIIB  CAT..GAGGT GTGTGTGGTT GAGACGCTGA TTC......C GATCTGGTCC
wSSIID  CAT..GAGGT GTGTGTGGTT GAGACGCTGA TTC......C AATCCGGCCC
wSSIIA  CATGAGAgGT GTGTGTGGTT GAGACGCTGA TTCCGATCTc gatctGGTCC
                                                              2750

        2751
wSSIIB  GTAGCAGAGT AGAGCGGGAGG CTCCTTGTTA CAGGTATATG
wSSIID  GTAGCAGAGT AGAGCGGGAGG TATATGGGAA TCTTAACTTG GTATTGTAAT
wSSIIA  GTAGCAGAGT AGAGCGGGACG CTCCTTGTTg CAGGTATATG
                                                              2800
```

# FIGURE 2N

```
                    2801                                           2850
          wSSIIB    GGAATGTTGT TAACTTGGTA TTGTAATTTG TTATGTTGTG TGCATTATTA
          wSSIID    TTGTTATGTT GTGTGCATTA TTACAATGTT GTTACTTATT CTTGTTAAGT
          wSSIIA    GGAATGTTGT CAACTTGGTA TTGTAgTTTG cTATGTTGTa TGCgTTATTA

                    2851                                           2900
          wSSIIB    CAGAGGGCAA CGATCTGCGC CGGCGCACCG GCCCAACTGT TGGGCCGGTC
          wSSIID    CGGAGGCCAA GGGCGAAAGC TAGCTCACAT GTCTGATGGA TGCAAAAAAA
          wSSIIA    caatgttgtt acttattctt gtTAAAAAAA AAAAAAAAAA AAAA~~~~~

                    2901                                           2950
          wSSIIB    GCACAGCAGC CGTTGGATCC GACCGCCTGG GCCGTTGGAT CCCACCGAAA
          wSSIID    AAAAAAAAAA AAA~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~
          wSSIIA    ~~~~~~~~~~ ~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~

                    2951        2965
          wSSIIB    AAAAAAAAAA AAAAA
          wSSIID    ~~~~~~~~~ ~~~~~
          wSSIIA    ~~~~~~~~~ ~~~~~
```

**FIGURE 20**

| |
|---|
| FIGURE 3A |
| FIGURE 3B |
| FIGURE 3C |
| FIGURE 3D |
| FIGURE 3E |
| FIGURE 3F |
| FIGURE 3G |

**FIGURE 3**

```
WSSIIA    1 MSSAVASAAS ---FLALASA SP-GRSRRRA RVSAPPPHAG AGRL----HW PPWPP-QRTA  51
WSSIIB    1 ********** --I-****** **-*******T ****-****S* ***-----** **S**-****  51
WSSIID      ---------- ---------- ---------- ---------- ---------- ----------
ZSSIIA    1 ****AV*SS* STF******* **G**--*** **GSS*F*T* *--S*SFAFWA **S**RAPRD  57
ZSSIIB    1 *PG*-I*SS* SAFL*PV**S **--R****G S*G*ALRSY* YSGAELRL** ARRG*P*DG*  56
PEASSII   1 *MLSLG*D*T VLP*H*KNLK FTPKL*TLNG --DLAFSKGL GVGRLNCGSV -------R  49
POTSSII  10 PVNFIFCDFY VMENSI*LHS GNQFHPNLPL --LALRPKK LSLIHGSSRE -------Q  57

                  ⇓ Transit peptide cleavage site

WSSIIA.  52 RDGGVAARAA GKKDARVDDD AASARQPRAR RGGAATKVAE RRDPVKTLDR DAAEGGAPAP 111
WSSIIB   52 ***A****** ******GI-** **P*****L ********** ********** *********S* 110
WSSIID      ---------- ---------- ---------- ---------- ---------- ----------
ZSSIIA   58 AALVR*EAE* *G***PPERS GDA**L**** *----NA*SK *----*---- ----------  97
ZSSIIB   57 -ASVR**A*P AGG------- ---------- ---------- ---------- ----------  68
PEASSII  50 LNHKQHV**V **SFGADENG DG*EDDVVNA TIEKSK**LA LQRELIQQIA ERKKLVSSID 109
POTSSII  58 MWRNQRVK*T *ENSGEAA-S *DESNDALQV TIEKSK**LA MQQDLLQQIA ERRKVVSSIK 116
```

**FIGURE 3A**

```
WSSIIA   112 PAPRQDAARP PSMNGTPVNG ENKSTGGGGA TKDSGLPAPA RAPHPSTQNR VPVNGENKAN 171
WSSIIB   111 *****ED**L *****M***** ********** ********** ***Q**S*** ********** 170
WSSIID       ---------- ---------- ---------- ---------- ---------- ----------
ZSSIIA    98 ---------- ---------- ----LQPVG RYG*ATGNT* *TGAA*C**A ALADV*I*SI 132
ZSSIIB    69 ---------- ---------- ---------- -ESEEAAKSS SSSQAGAVQG STAKAVDS*S  97
PEASSII  110 SDSIPGLEGN GVSYESSEKS LSR------- ---------- ------DS*P QKGSSSSGSA 146
POTSSII  117 S----SL*NA KGTYDGGSGS LSDVDIPDVD KDYNVTVPST A*TGITDVDK NTPPAISHDF 172


WSSIIA   172 VASPPTSIAE VVAPDSAATI SISDKAPESV VPAEKPPPSS GSNFVVSASA PRLDIDSDVE 231
WSSIIB   171 ********** *A***P**** ********** *****A**** *****P**** *GS*TV**** 230
WSSIID   203 ---------- ---------- ---------- -****T**** -****ES**** *GS*TV**** 231
ZSSIIA   134 **A*****VK FP**GYRMIL PSG*I***T* L**P**--LH E*PA*DGD*N --GIAPPT** 188
ZSSIIB    99 PPN*L**APK QSQSAAMQNG TSGGSSASTA A*VSG*KADH P*AP*TKREI DASAVKPEPA 158
PEASSII  147 *ETKR--WHC FQQ-----LC RSKETETWA* SSVGINQGFD EIEKKND*VK ASSKLHFNEQ 199
POTSSII  173 *E*KREIKRD LADERAPPLS RS*IT*SSQI SSTVSSK--R TL*VPPETPK SSQETLL**N 230
```

**FIGURE 3B**

```
                                                                    wSSIIp1 Region
WSSIIA. 232 PELKKGAVIV EEAPNPKALS PPAAPAVQED LWDFKKYIGF EEPVEAKDDG WAVADDAGSF 291
WSSIIB  231 L********* K********* ********** ********** ********** R********* 290
WSSIID  232 Q*****V*** ****K***** ********** ********** ********** R********* 291
ZSSIIA  189 *--------- I--------- ----L***A  T********* D**D****S  RVG******* 224
ZSSIIB  159 GDDARPVESI ---------- ---------- -------*I  A***D*A*-  A*P*T**AAS 188
PEASSII 200 IKN*LYERPD TKDIS--SSI R--------- ---------- KFENFEGANE PSSKEV*NEA 242
POTSSII 231 SRKSLVD*PG KKIQSYMPSL R--------- ----*ESSAS HVEQRNENLE GSS*EANEET 277

                       Region 1                      Region 2
WSSIIA. 292 EHHQNHD--S GPLAGENVMN VVVVAAECSP WCKTGGLGDV AGALPKALAK RGHRVMVVVP 349
WSSIIB  291 ****-*---* ********** ********** ********** ********** ********** 348
WSSIID  292 ****-*---* ********** ********** ********** ********** ********** 349
ZSSIIA  225 **YGDN*--* ********** **I******* V********* V********R **********R 282
ZSSIIB  189 APYDRE*NEP ******P*** *****S**A* F********* V*********I* *********I* 248
PEASSII 243 *NFESGGEKP P*****T*** IIL*S***A* *S******** **S*****R **********R 302
POTSSII 278 *DPV*I*EKP P*****T*** IIL**S***A* *S******** **S*****R **********R 337
```

FIGURE 3C

Sgp-1 Peptide 3

```
WSSIIA  350  RYGDYEEAYD VGVRKYYKAA GQDMEVNYFH AYIDGVDFVF IDAPLFRHRQ EDIYGGSRQE  409
WSSIIB  349  ********** ********** ********** ********** ********** **********  408
WSSIID  350  **-*****PT* ********** ********** *********E ********** **********  409
ZSSIIA  283  ***-**V*F* **I****** **L****** ***F****** D********** **********  342
ZSSIIB  249  ***E*A**R* L***RR**V* ****S***T*** VE**P****H S*********** NN****E*LD  308
PEASSII 303  H**N*A**H* I****R**V* ****T******I** *S*I**NLE T******I** SN****N*LD  362
POTSSII 338  **DN*P*PQ* S****I**VD ***VD*T**Q *LLMDC**** *HSHM***IG NN****N*VD  397
```

Region 3

```
WSSIIA  410  IMKRMILFCK AAVEVPWHVP CGGVPYGDGN LVFIANDWHT ALLPVYLKAY YRDHGLMQYT  469
WSSIIB  409  ********** ********** ********** ********** ********** **********  468
WSSIID  410  ********** V********* ****C***** ********** ********** **********  469
ZSSIIA  343  ****V***** ********** ****C***** ********** ********** **********  402
ZSSIIB  309  *L******** ***TV*****YA* ****TV***** ****N***** ***N*****A  368
PEASSII 363  *LR*V***** *IC******* ********** ****N**** *****N**  422
POTSSII 398  *L***V***** **I******* ****C***** ****A****** *N*I*N**  457
```

## FIGURE 3D

```
WSSIIA  470 RSIMVIHNIA HQGRGPVDEF PFTELPEHYL EHFRLYDPVG GEHANYFAAG LKMADQVVVV 529
WSSIIB  469 ********** ********** ********** ********** ********** ********** 528
WSSIID  470 ********** ********** ********** ********** ********** ********** 529
ZSSIIA  404 **VL****** ****YMD*** Q**E****** ****I***** *****I**** *R**T*    462
ZSSIIB  369 **VL*****D* *****I**** D**K***NI* VNFD****I* *D*S*V**** *T*R**T*  428
PEASSII 423 **VL****ED* NTVD*SGN** DL*KM***** ***F*I**** *T**RI*T*          482
POTSSII 458 **VL****LED* SYVD**P**M DP*K****** ***F*I**** *T**R**T*         517

                               Region 4

WSSIIA  530 SPGYLWELKT VEGGWGLHDI IRQNDWKTRG IVNGIDNMEW NPEVDVHLK- SDGYTNFSLG 588
WSSIIB  529 ********** ********** ********** ********** *****-     *          587
WSSIID  530 ********** ********** ********** *****A**** -          ****R     588
ZSSIIA  463 *R******** **S*****IN* **S***IN* **K*****R-            *Y**E     521
ZSSIIB  429 *N**M***** S********* *N*****LQ* *******MS** **A*****H- **D***YTFE 487
PEASSII 483 *H**A***** S*******N* *NES***F** ***V*TKD* **QF*AY*T- ****YN*K   541
POTSSII 518 *H**S***** SQ*****Q* *NE****LQ* ***L***TK** ***PR     ****M*Y**D 577
```

**FIGURE 3E**

```
                     Region 5                                           Region 5a
WSSIIA  589 TLDSGKRQCK EALQRELGLQ VRADVPLLGF IGRLDGQKGV EIIADAMPWI VSQDVQLVML 648
WSSIIB  588 ********** ********** **G******* ********** ********** ********** 647
WSSIID  588 ********** ********** ********** ********** ********** ********** 648
ZSSIIA  522 ***A****** A*******E **D******* ********** D**G****** AG******** 581
ZSSIIB  488 ***T****** A****Q**** **D****I** *********H** D****IH** AG******** 547
PEASSII 542 **QT****** A*******P **E***IIS* *****H**** DL**E*I**M M*H******* 601
POTSSII 578 **QT**P*** A***K****P **D****I** *****P**** DL**E*V**M MG******** 637

                     Region 6
WSSIIA  649 GTGRHDLESM LRHFEREHHD KVRGWVGFSV RLAHRITAGA DALLMPSRFE PCGLNQLYAM 708
WSSIIB  648 *********G* ********** ********** ********** ********** ********** 707
WSSIID  649 *********** *Q******** ********** ********** *****V**** ********** 708
ZSSIIA  582 ***A**R*** *Q*L****PN PM******** ********** *V*V****** ********** 641
ZSSIIB  548 ***A***D* **R**S**S* P********* ***A****** *I******** ********** 607
PEASSII 602 ****A***Q* *KE**AQ*C* *I*S****** KM*****S* *I******** ********** 661
POTSSII 638 ****R***Q* **Q**CQ*N* *I******** KTS******* *I******** **A******* 697
```

**FIGURE 3F**

```
                           Region 7
WSSIIA  709 AYGTVPVVHA VGGVRDTVPP FDPFNHSGLG WTFDRAEAHK LIEALGHCLR TYRDYKESWR 768
WSSIIB  708 ********** ***L****** ********** *******Q** ********** ********** 767
WSSIID  709 ********** ***L****** ********** ********** ********** ****E***** 768
ZSSIIA  642 ********** ***L***A** ****GDA*** *******N** ****R****D **K*G***K  701
ZSSIIB  608 ********** ***L***A** *****DT*** *******NR M*D**S***T ****N*****  667
PEASSII 662 S*****G    ***L****Q* *N*DE**V*  *******N*  *MA**WN**L **K****K**E 721
POTSSII 698 K***I***** ***L****Q* **LMSQDW*  GPS*****SQ **PRIRN**L ***E**K**E  757


WSSIIA  769 GLQERGMSQD FSWEHAAKLY EDVLLKAKYQ W 799
WSSIIB  768 ********** ********** **V******* * 798
WSSIID  769 ********** ********** **V******* * 799
ZSSIIA  702 S**A****** L**D**E*** **V******* * 732
ZSSIIB  668 ACRA***AE* L**D***V** **V******* * 698
PEASSII 722 *I******** L**DN**QQ* *E**VA**** * 752
POTSSII 759 *I*T*C*T** L**DN**QN* *E**IA**** * 788
```
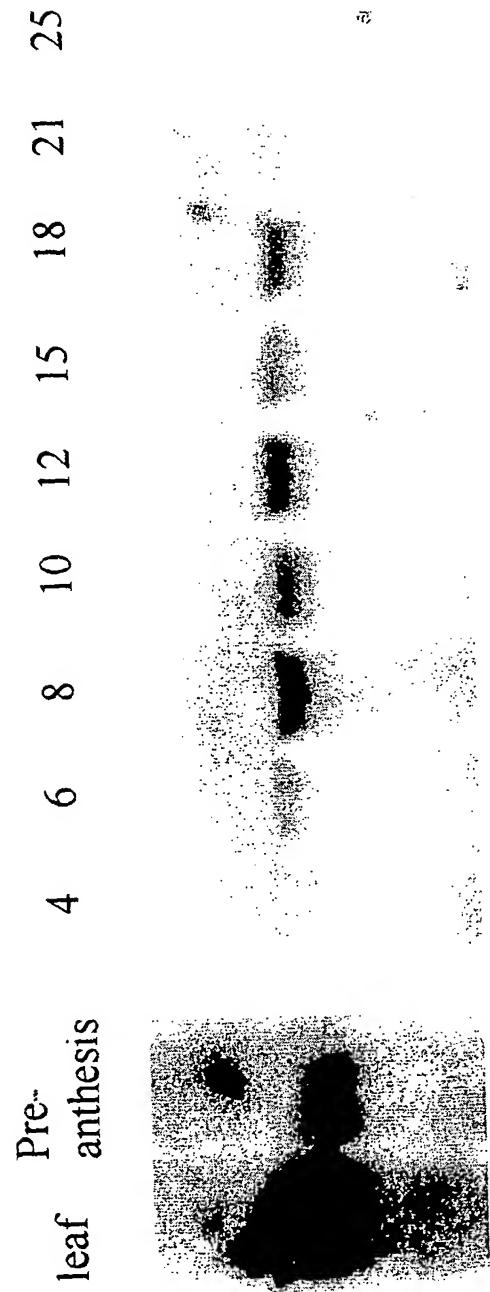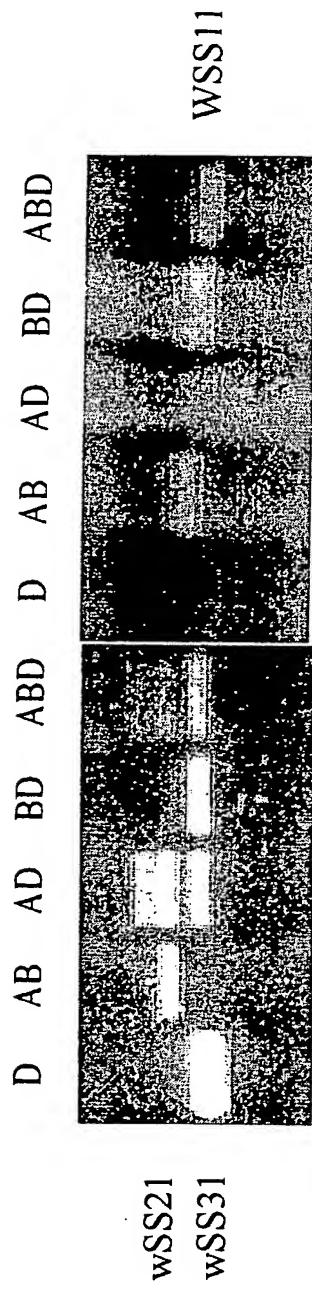
## FIGURE 3G
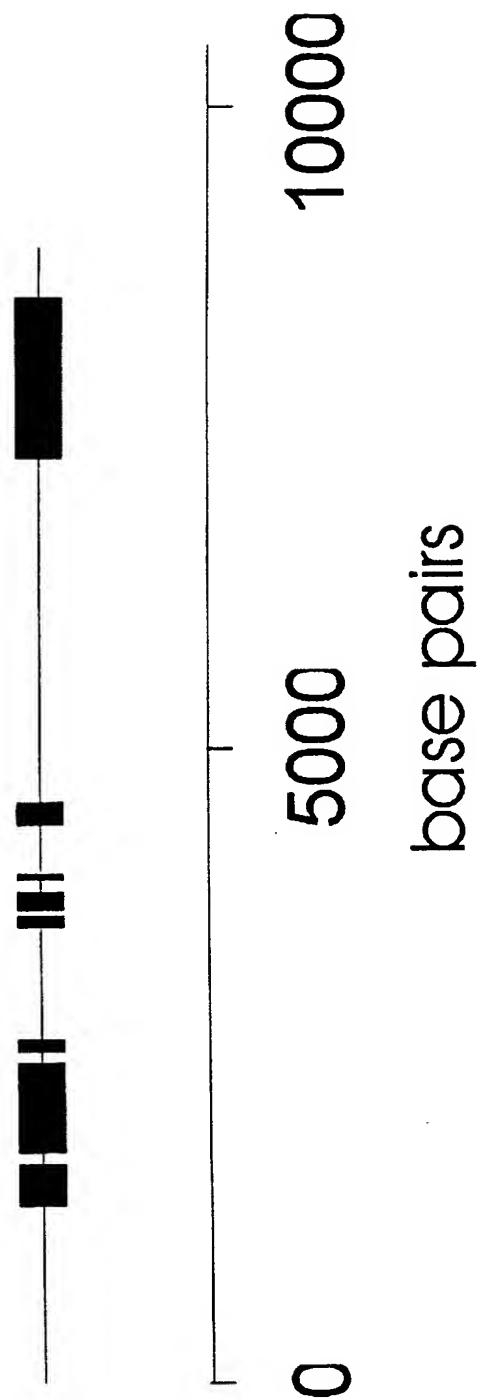
FIGURE 4

**FIGURE 5**

**FIGURE 6**

| |
|---|
| FIGURE 7A |
| FIGURE 7B |
| FIGURE 7C |
| FIGURE 7D |
| FIGURE 7E |
| FIGURE 7F |
| FIGURE 7G |
| FIGURE 7H |
| FIGURE 7I |

**FIGURE 7**

```
        1                                                          50
wSSIII  MEMSLWPRSP LCPRSRQPLV VVRP..AGRG GLTQPFLMNG RFTRSRTLRC
mSSIII  MEMVLRSQSP LCLRS.GPVL IFRPTVAGGG GGTQSLLRTT RFARRVIRC
pSSIII  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~

        51                                                        100
wSSIII  MVASSDPPNR KSRRMVPPQV KVISSRGYTT RLIVEPSNEN TEHNNRD...
mSSIII  VVASPGCPNR KS.RTASPNV KVAAYSNYAP RLLVESSSKK SEHHDSSRHR
pSSIII  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~

        101                                                       150
wSSIII  EETLDTYNAL LSTETAEWTD NREAE..... ..TAKADSSQ NALSSSIIGE
mSSIII  EETIDTYNGL SGSDAAELTS NRDVEIEVDL QHISEEELPG KVSINASLGE
pSSIII  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~

        151                                                       200
wSSIII  VDVAD..... EDILAADLTV YSLSSVMKKE VDAADKARVK EDAFELDLPA
mSSIII  METVDEAEVE EDKFEVDTSG IVLRNVAVRE VDPKDEHNAK .DVFVVDSSG
pSSIII  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
```

FIGURE 7A

```
        201                                              250
wSSIII  TTLRSVIVDV MDHNGTVQET LRSVIVDVMD .HNGTVQE.. TLRSVIVDVM
mSSIII  TAPDNAAVEE VVDEAEVEED MVDVDILGLD LNNATIEEID LMEEALLENF
pSSIII  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

        251                                              300
wSSIII  D.DAADKARV EEDVFELDLS GNISSSAT.. .......... .....TVEL
mSSIII  DVDSPGNASS GRTYGGVDEL GELPSTSVDC IAINGKRRSL KPKPLPIVRF
pSSIII  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

        301                                              350
wSSIII  DAVDEVGPVQ DKFEATSSGN VSNSATVREV DASDE...AG NDQGIFRADL
mSSIII  QEQEQIVLSI VDEEGLIASS CEEGQPVVDY DKQEENSTAF DEQKQLTDDF
pSSIII  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

        351                                              400
wSSIII  SGNVFSSSTT VEVG..AVDE AGSIKDRFET DSSGNVSTSA PMWDAIDETV
mSSIII  PEEGISIVHF PEPNNDIVGS SKFLEQKQEL DGSYKQDRST TGLHEQDQSV
pSSIII  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
```

**FIGURE 7B**

```
            401                                                  450
    wSSIII  ADQDTFEADL  SGNASSCATY  REVDDVVDET  RSEEETFAMD  LFASESGHEK
    mSSIII  VSSHGQDKSI  VG.VPQQIQY  NDQSIAGSHR  QDQSIAGAPE  QIQSVAGYIK
    pSSIII  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~~~~~~~  ~~~~MDVPF

            451                                                  500
    wSSIII  HMAVDYVGEA  TDEEETYQQQ  YPVPSSFSMW  DKAIAKTGVS  LNPELRLVRV
    mSSIII  PNQ.SIVGSC  KQHELIIPEP  KKIESIISYN  EIDQSIVGSH  KQDKSVVSVP
    pSSIII  PLHRSLSCTS  VSNAITHLKI  KPILGFVSHG  TTSLSVQSSS  WRKDGMVTGV

            501                                                  550
    wSSIII  EEQGKVNFSD  KKDLSIDDLP  GQNQSIIGSY  KQDKSIADVA  GPTQSIFGSS
    mSSIII  EQIQSIVSHS  KPNQSTVDSY  RQAESIIGVP  EKVQSITSYD  KLDQSIVGSL
    pSSIII  SFSICANFSG  RRRRKVSTPR  SQGSSPKGFV  PRKPSGMSTQ  RKVQKSNGDK

            551                                                  600
    wSSIII  KQHRSIVAFP  KQNQSIVSVT  EQKQSIVGFR  SQDLSAVSL.  ........P
    mSSIII  KQDEPIISVP  EKIQSIVHYT  KPNQSIVGLP  KQQQSIVHIV  EPKQSIDGFP
    pSSIII  ESKSTSTSKE  SEISNQKTVE  ARVETSDDDT  KGVVRDHKFL  EDEDEINGST
```

**FIGURE 7C**

```
       601                                          650
wSSIII KQ.NVPIVGT SREGQTKQVP VVDRQDALYV NGLEAKEGDH TSEKTDEDAL
mSSIII KQ.DLSIVGI SNEFQTKQLA TVGTHDGLLM KGVEAKE... TSQKTEGDTL
pSSIII KSISMSPVRV SSQFVESEET GGDDKDAVKL N..KSKRSEE SGFIIDSVIR

       651                                          700
wSSIII HVKFNVDNVL RKHQADRTQA VEKKTWKKVD EEHLYMTEHQ KRAA..EGQM
mSSIII QATFNVDNLS QKQEGLTKEA DEITIIEKIN DEDLVMIEEQ KSIAMNEEQT
pSSIII EQSGSQGETN ASSKGSHAVG TKLYEILQVD VEPQQLKEN. .NAGNVEYKG

       701                                          750
wSSIII VVNEDELSIT EIGMGRGD.K IQHVLSEEEL SWSEDEVQLI EDDGQYEVDE
mSSIII IVTEEDIPMA KVEIGIDKAK FLHLLSEEES SWDENEVGII EADEQYEVDE
pSSIII PVASKLLEIT KA......SD VEHTESNEID DLDTN..SFF KSDLIEEDEP

       751                                          800
wSSIII TSVSVNVEQD IQGSPQDVVD PQALKVMLQE LAEKNYSMRN KLFVFPEVVK
mSSIII TSMS..TEQD IQESPNDDLD PQALWSMLQE LAEKNYSLGN KLFTYPDVLK
pSSIII LAAGTVETGD SSLNLRLEME ANLRRQAIER LAEENLLQGI RLFCFPEVVK
```

**FIGURE 7D**

```
                                                                 850
801
wSSIII   ADSVIDLYLN RDLTALANEP DVVIKGAFNG WKWRLFTERL HKSDLGGVWW
mSSIII   ADSTIDLYFN RDLSAVANEP DVLIKGAFNG WKWRFFTEKL HKSELAGDWW
pSSIII   PDEDVEIFLN RGLSTLKNES DVLIMGAFNE WRYRSFTTRL TETHLNGDWW

                                                                 900
851
wSSIII   SCKLYIPKEA YRLDFVFFNG RTVYENNGNN DFCIGIEGTM NEDLFEDFLV
mSSIII   CCKLYIPKQA YRMDFVFFNG HTVYENNNNN DFVIQIESTM DENLFEDFLA
pSSIII   SCKIHVPKEA YRADFVFFNG QDVYDNNDGN DFSITVKGGM QIIDFENFLL

                                                                 950
901
wSSIII   KEKQRELEKL AMEEAERRTQ TEEQRRRKEA RAADEAVRAQ AKAEIEIKKK
mSSIII   EEKQRELENL ANEEAERRRQ TDEQRRMEEE RAADKADRVQ AKVEVETKKN
pSSIII   EEKWREQEKL AKEQAERERL AEEQRRIEAE KAEIEADRAQ AKEEAAKKKK

                                                                1000
951
wSSIII   KLQSMLSLAR TCVDNLWYIE ASTDTRGDTI RLYYNRNSRP LAHSTEIWMH
mSSIII   KLCNVLGLAR APVDNLWYIE PITTGQEATV RLYYNINSRP LVHSTEIWMH
pSSIII   VLRELMVKAT KTRDITWYIE PSEFKCEDKV RLYYNKSSGP LSHAKDLWIH
```

**FIGURE 7E**

```
                  1001                                                      1050
wSSIII   GGYNNWTDGL  SIVESFVKCN  DKDGDWWYAD  VIPPEKALVL  DWVFADGPAG
mSSIII   GGYNNWIDGL  SFAERLVHHH  DKDCDWWFAD  VVVPERTYVL  DWVFADGPPG
pSSIII   GGYNNWKDGL  SIVKKLVKSE  RIDGDWWYTE  VVIPDQALFL  DWVFADGPPK

                  1051                                                      1100
wSSIII   NARNYDNNAR  QDFHAILPNN  NVTEEGFWAQ  EEQNIYTRLL  QERREKEETM
mSSIII   SARNYDNNGG  HDFHATLP.N  NMTEEEYWME  EEQRIYTRLQ  QERREREEAI
pSSIII   HAIAYDNNHR  QDFHAIVP.N  HIPEELYWVE  EEHQIFKTLQ  EERRLREAAM

                  1101                                                      1150
wSSIII   KRKAERSANI  KAEMKAKTMR  RFLLSQKHIV  YTEPLEIRAG  TTVDVLYNPS
mSSIII   KRKAERNAKM  KAEMKEKTMR  MFLVSQKHIV  YTEPLEIHAG  TTIDVLYNPS
pSSIII   RAKVEKTALL  KTETKERTMK  SFLLSQKHVV  YTEPLDIQAG  SSVTVYYNPA

                  1151                                                      1200
wSSIII   NTVLNGKSEG  WFRCSFNLWM  HSSGALPPQK  MVKSGDGPLL  KATVDVPPDA
mSSIII   NTVLTGKPEV  WFRCSFNRWM  YPGGVLPPQK  MVQAENGSHL  KATVYVPRDA
pSSIII   NTVLNGKPEI  WFRCSFNRWT  HRLGPLPPQK  MSPAENGTHV  RATVKVPLDA
```

**FIGURE 7F**

```
         1201                                                      1250
wSSIII   YMMDFVFSEW  EEDGIYDNRN  GMDYHIPVSD  SIETENYMRI  IHIAVEMAPV
mSSIII   YMMDFVFSES  EEGGIYDNRN  GLDYHIPVFG  SIAKEPPMHI  VHIAVEMAPI
pSSIII   YMMDFVFSER  EDGGIFDNKS  GMDYHIPVFG  GVAKEPPMHI  VHIAVEMAPI

         1251                                                      1300
wSSIII   AKVGGLGDVV  TSLSRAIQDL  GHTVEVILPK  YDCLNQSSVK  DLHLYQSFSW
mSSIII   AKVGGLGDVV  TSLSRAVQDL  GHNVEVILPK  YGCLNLSNVK  NLQIHQSFSW
pSSIII   AKVGGLGDVV  TSLSRAVQDL  NHNVDIILPK  YDCLKMNNVK  DERFHKNYFW

         1301                                                      1350
wSSIII   GGTEIKVWVG  RVEDLTVYFL  EPQNGMFGVG  CVYG.RNDDR  RFGFFCHSAL
mSSIII   GGSEINVWRG  LVEGLCVYFL  EPQNGMFGVG  YVYG.RDDDR  RFGFFCRSAL
pSSIII   GGTEIKVWFG  KVEGLSVYFL  EPQNGLFSKG  CVYGCSNDGE  RFGFFCHAAL

         1351                                                      1400
wSSIII   EFLLQNEFSP  HIIHCHDWSS  APVAWLYKEH  YSQSRMASTR  VVFTIHNLEF
mSSIII   EFLLQSGSSP  NIIHCHDWSS  APVAWLHKEN  YAKSSLANAR  VVFTIHNLEF
pSSIII   EFLLQGGFSP  DIIHCHDWSS  APVAWLFKEQ  YTHYGLSKSR  IVFTIHNLEF
```

**FIGURE 7G**

```
            1401                                                    1450
wSSIII      GAHYIGKAMT YCDKATTVSP TYSRDVAGHG AIAPHREKFY GILNGIDPDI
mSSIII      GAHHIGKAMR YCDKATTVSN TYSKEVSGHG AIVPHLGKFY GILNGIDPDI
pSSIII      GADLIGRAMT NADKATTVSP TYSQEVSGNP VIAPHLHKFH GIVNGIDPDI

            1451                                                    1500
wSSIII      WDPYTDNFIP VPYTCENVVE GKRAAKRALQ QKFGLQQTDV PIVGIITRLT
mSSIII      WDPYNDNFIP VHYTCENVVE GKRAAKRALQ QKFGLQQIDV PVVGIVTRLT
pSSIII      WDPLNDKFIP IPYTSENVVE GKTAAKEALQ RKLGLKQADL PLVGIITRLT

            1501                                                    1550
wSSIII      AQKGIHLIKH AIHRTLESNG HVVLLGSAPD HRIQGDFCRL ADALHGVYHG
mSSIII      AQKGIHLIKH AIHRTLERNG QVVLLGSAPD SRIQADFVNL ANTLHGVNHG
pSSIII      HQKGIHLIKH AIWRTLERNG QVVLLGSAPD PRVQNNFVNL ANQLHSKYND

            1551                                                    1600
wSSIII      RVKLVLTYDE PLSHLIYAGS DFIIVPSIFE PCGLTQLVAM RYGSIPIVRK
mSSIII      QVRLSLTYDE PLSHLIYAGS DFILVPSIFE PCGLTQLVAM RYGTIPIVRK
pSSIII      RARLCLTYDE PLSHLIYAGA DFILVPSIFE PCGLTQLTAM RYGSIPVVRK
```

**FIGURE 7H**

```
            1601                                                      1650
wSSIII   TGGLHDTVFD   VDNDKDRARS   LGLEPNGFSF   DGADSNGVDY   ALNRAIGAWF
mSSIII   TGGLFDTVFD   VDNDKERARD   RGLEPNGFSF   DGADSNGVDY   ALNRAISAWF
pSSIII   TGGLYDTVFD   VDHDKERAQQ   CGLEPNGFSF   DGADAGGVDY   ALNRALSAWY

            1651                                                      1689
wSSIII   DARDWFHSLC   KRVMEQDWSW   NRPALDYIEL   YHAARKF*~
mSSIII   DARSWFHSLC   KRVMEQDWSW   NRPALDYIEL   YRSASKL~~
pSSIII   DGRDWFNSLC   KQVMEQDWSW   NRPALDYLEL   YHAARKLE*
```

**FIGURE 7I**

**[a] Wyuna**
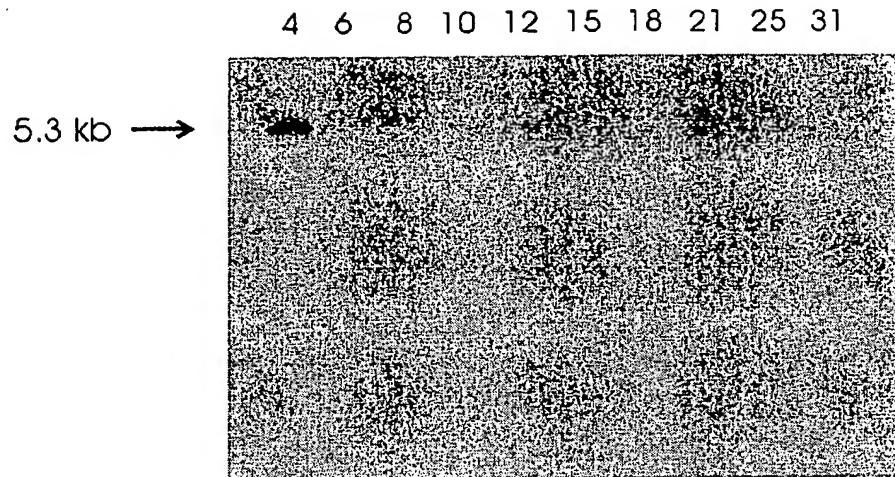


**[b] Gabo**                               **[c] Gabo**



**FIGURE 8**

FIGURE 9B
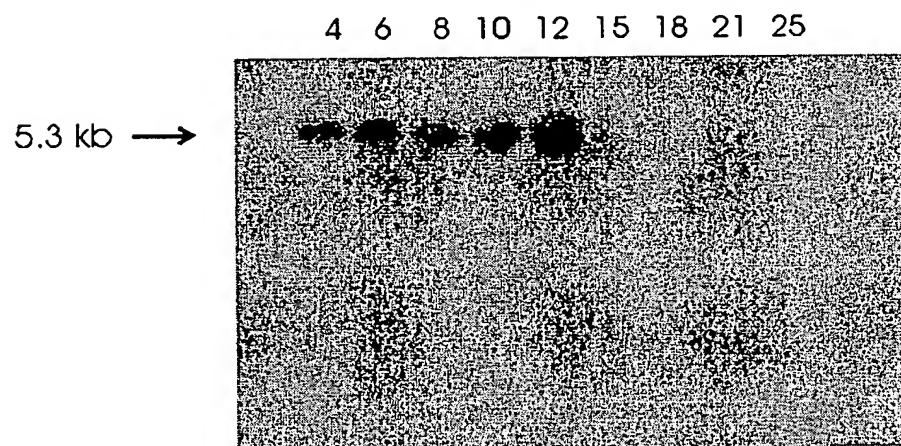
FIGURE 9D
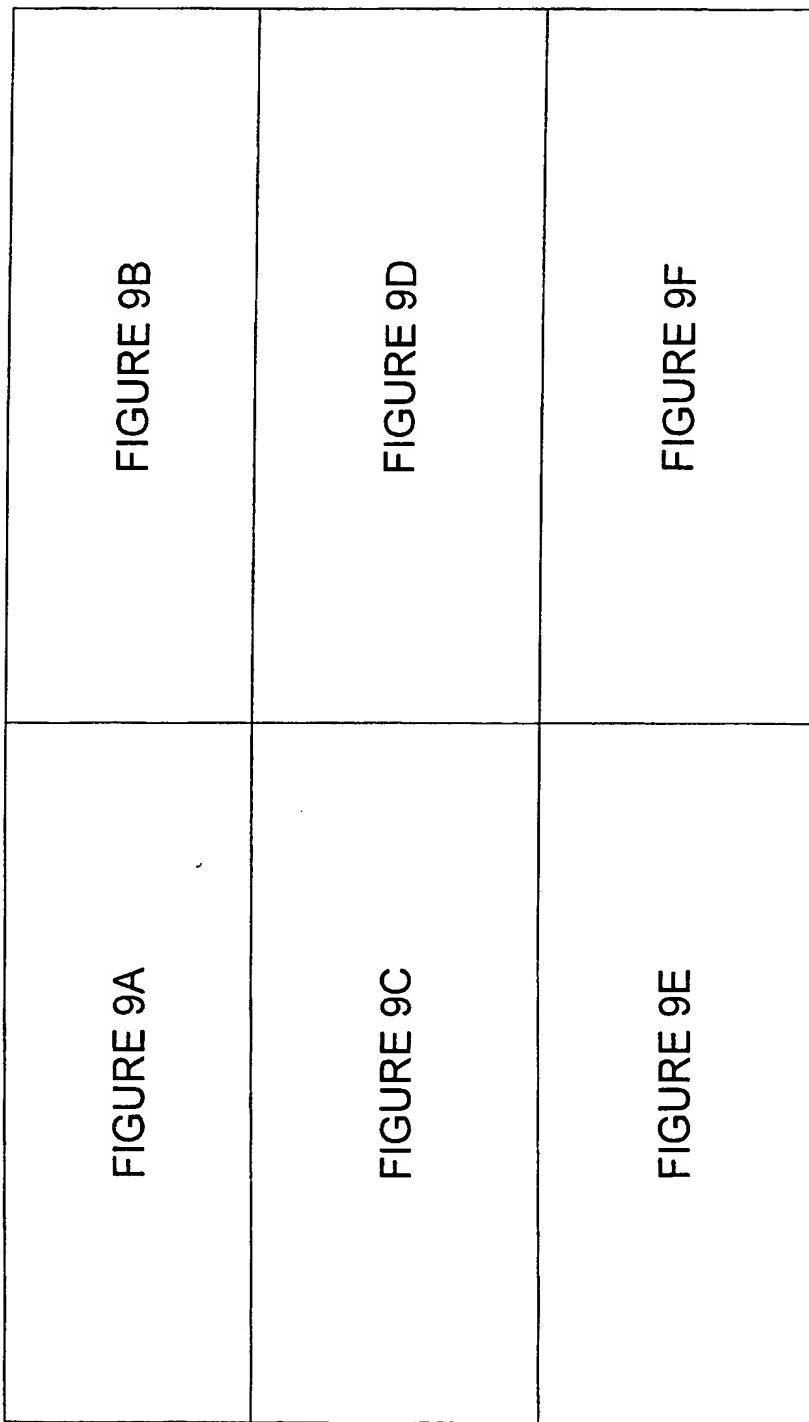
FIGURE 9F

FIGURE 9A

FIGURE 9C

FIGURE 9E

**FIGURE 9**

```
                              Region 1                        Region 2
                  10        20        30        40        50
wGBSS   81 FVGAEMAPWS KTGGLGDLLG GLPPAMAANG HRVMVISPRY DQYKDAWDT-
wSS1   144 -*TG*A**YA *S*****VC* S**I*L**R* *****VM*** LNGSSDKNYA
wSS2   314 --A**CS**C *********VA* A**K*L*KR* *****VV*** GD*EE*Y*V-
wSS3  1187 -IAV****VA *V*****VVT S*SR*IQDL* *T*E*L*K* *CLNQSSVK-

                 100       110       120       130       140
wGBSS  171 LEKVRGKTKE KIYGPDAGTD YEDNQQRFSL LCQAALEVPR ILNLDNNPYE
wSS1   234 -HRPGSLYGD -----NFGA FG***F*YT* **Y**C*A*L **E*GGYI*G
wSS2   404 RHRQEDIYGG -------S RQEIMK*MI* F*K**V***W HVPCGGV**G
wSS3  1277 **PQN*MFGV ------GCVY GRNDDR**GF F*HS***--F **QNEFS*H-

                 190       200       210       220       230
wGBSS  261 FCIHNISYQG RESEDDFAQL NLPD-----R FKSSFDEIDG YDKPVEGRKI
wSS1   324 LV***LAH** LEPASTYPD* G**PEWYGAL EWVFPEWARR HALDKGEAVN
wSS2   494 MV*****AH** *GPV*E*PFT E**------ -EHYLEHFRL **PVGGEHAN
wSS3  1367 *T***L-EF* AHYIGKAMTY CDK------ ---------- ----------
```

FIGURE 9A

```
           60         70          80         90
      ----SVVSE IKVVDKYERV RYFHCYKRGV DRVFVDHPCF   170
      KALYTGKHIK *PCFGGSHE* TF**E*RDN* *W*****SY    233
      ----G*RKY Y*AAGQDME* N***A*ID** *F**I*A*L*    403
      --------- -DLHLYQSFS WGGTEI*VW* G**EDLTVY*   1276

           Region 3
          150        160        170        180
      SGPYGEDVVF VCNDWHTGLL ACYLKSNYQS NGIYRAAKVA   260
      QN-----CM* *V****AS*V PVL*AAK*RP Y*V**DSRST    323
      D*-----NL** IA******A** PV***AY*RD H*LMQYTRSI   493
      --------II H*H**SSAPV *WLY*EH*SQ -SRMASTR*V   1366

          240        250        260        270
      NWMKAGILQA DKVLTVSPYY AEELISGEAR GCELDNIMRL   350
      FLKG*VVTAD RI*TVSQG*S W*VTTAEGGQ *LNELLSS*K    413
      YFAAGLKMAD QV*VVSPG*L W*LKTVEGGW *LHDIIRQND    583
      --------- --AT TVSPTYSRDV AGHGAIAPHR   1456
```

**FIGURE 9B**

```
                Region 4
         280        290        300        310        320
wGBSS 351 TGITTIVNGM DVSEWDPTKD KFLAVNYDIT TALEGKALNK EALEGKALNK
wSS1  414 SVLNG*****I *IND*N**T* *C*PHH*SV- ---------- DD*S***KC*
wSS2  584 WKTRG*****I *NM**N*EV* VH*KSDGYTN -----FSLG TLDS**RQC*
wSS3  1457 EKFYG*L**I *PDI***YT* N*IP*P*TCE ----NVVEG* **AKRALQQ*

                Region 5a
         370        380        390        400        410
wGBSS 441 LKEEDVQIVL LGTGKKKFER LLKSIEEKFP SKVRAVVRFN ------APLA
wSS1  504 *MR*****F*M **S*DPI**G WMR*T*SSYK D*F*GW*G*S ------V*VS
wSS2  674 V-SQ***L*M *****RHDL*S M*RHF*REHH D***GW*G*S ------VR**
wSS3  1547 TL*SNG*V** **SAPDHRIQ GDFCRLADAL HG*YHGRVKL -VLTYDE**S
```

FIGURE 9C

```
        Region 5
  330        340        350        360
EALQAEVGLP VDRKVPLVAF IGRLEEQKGP DVMIASIPEI  440
AE**K*L*** *RED***IG* ****DY***I *LIKMA**+-  503
****R*L**Q *RAD***LG* ****DG***V EIIADAM*W*  673
FG**QT---- ---D**I*GI *T**TA***I -HL*KHAIHR  1546

        Region 6                              Region 7
  420        430        440        450
HQMMAGADVL AVTSRFEPCG LIQLQGMRYG TPCACASTGG  530
*RIT**C*I* LMP******* *N**YA*Q** *VPVVHG***  593
*RIT***A* LMP******* *N**YA*A** *VPVVHAV**  763
*LIY**S*FI I*P*I***** *T**VA**** SIPIVRK***  1636
```

## FIGURE 9D

```
Region 7 (Continued)
          460        470        480        490        500
wGBSS 531 LVDTIVEGKT GFHMGRLSYD CNVVEPADVK KVVTTLKRAV KVVGTPAYIIE
wSS1  594 *R**-**TEN ---------- --PFGAKGEE GTGWAFSPLT VDKMLW*LRT
wSS2  764 VR**-*PPFD ---------- --PFNHSGLG --W*FD**E AHKLIE*LGH
wSS3 1637 ****-*FD\) NDKDRAR*LG LEPNGFSFDG ADSNGVDY*L NRAIGAWFDA

          550        560        570        580        590        600
wGBSS 621 APLAMENVAA P*........ .......... .......... .......... ..........
wSS1  684 FVDQPYVM.. .......... .......... .......... .......... ..........
wSS2  854 KYQW...... .......... .......... .......... .......... ..........
wSS3 1727 .......... .......... .......... .......... .......... ..........
```

**FIGURE 9E**

```
                    510        520         530         540

MVKNCMIQDL SWKGPAKNWE DVLLELGVEG SEPGIVGEEI    620
AMSTFREHKP **E*LM*RGM TKDHTWDHAA EQYEQIF*WA    683
CLRTYRDYKE **R*LQERGM SQDFSWEHAA KLYED*LLKA    853
RDWFHSLCKK VMEQDWSWNR PA*DYIELYH AARKF*.....   1726

                    610        620         630

                    .......... .......... .......... .    710
                    .......... .......... .......... .    773
                    .......... .......... .......... .    943
                    .......... .......... .......... .   1816
```

**FIGURE 9F**

maizeGBSS

riceGBSS

wheatGBSS

potatoGBSS

peaGBSS

maizeSSI

riceSSI

wheatSSI

potatoSSI

wheatSSIIB

wheatSSIID

wheatSSIIA

maizeSSIIa

maizeSSIIb

peaSSII

potatoSSII

maizeSSII

wheatSSIII

potatoSSIII

GS
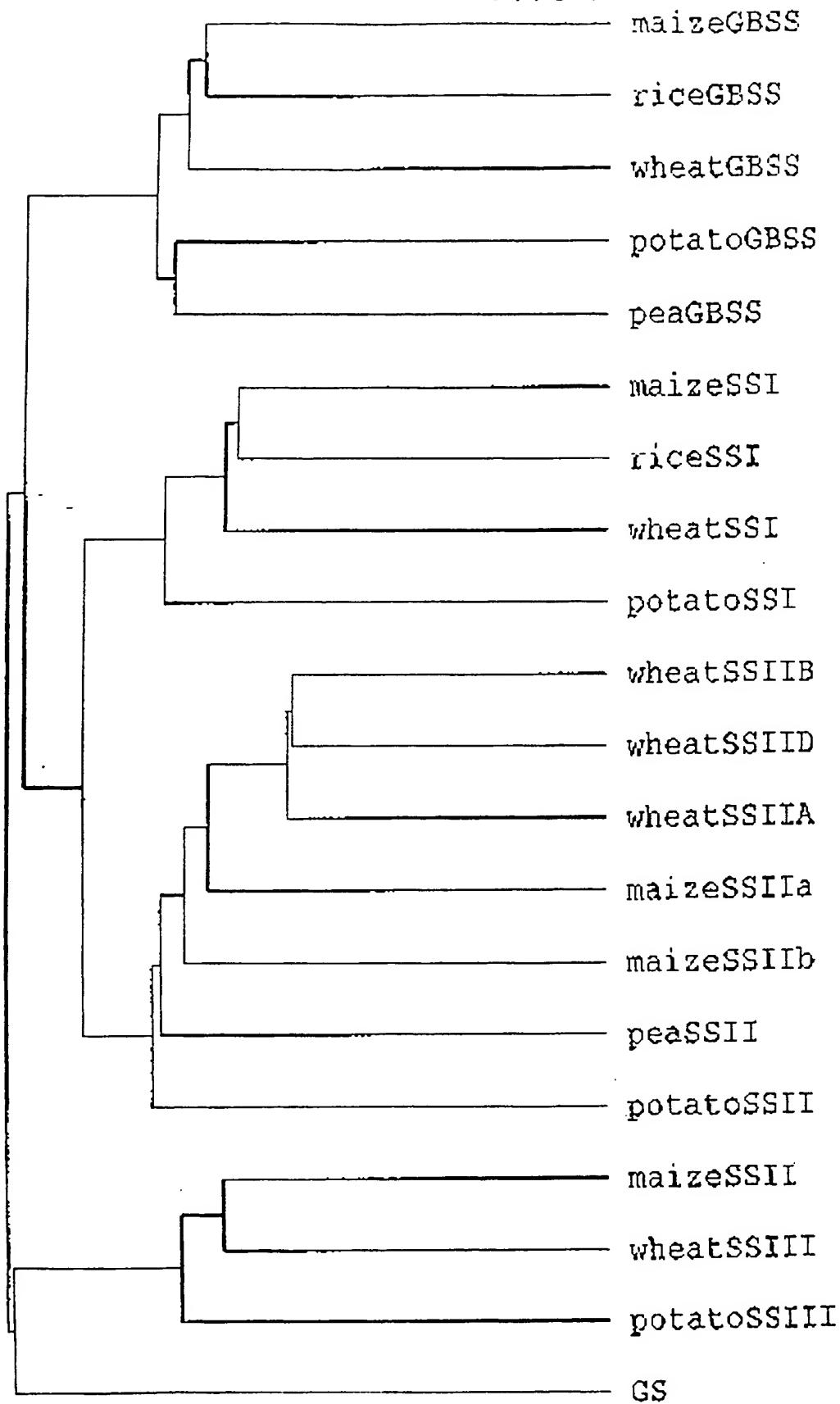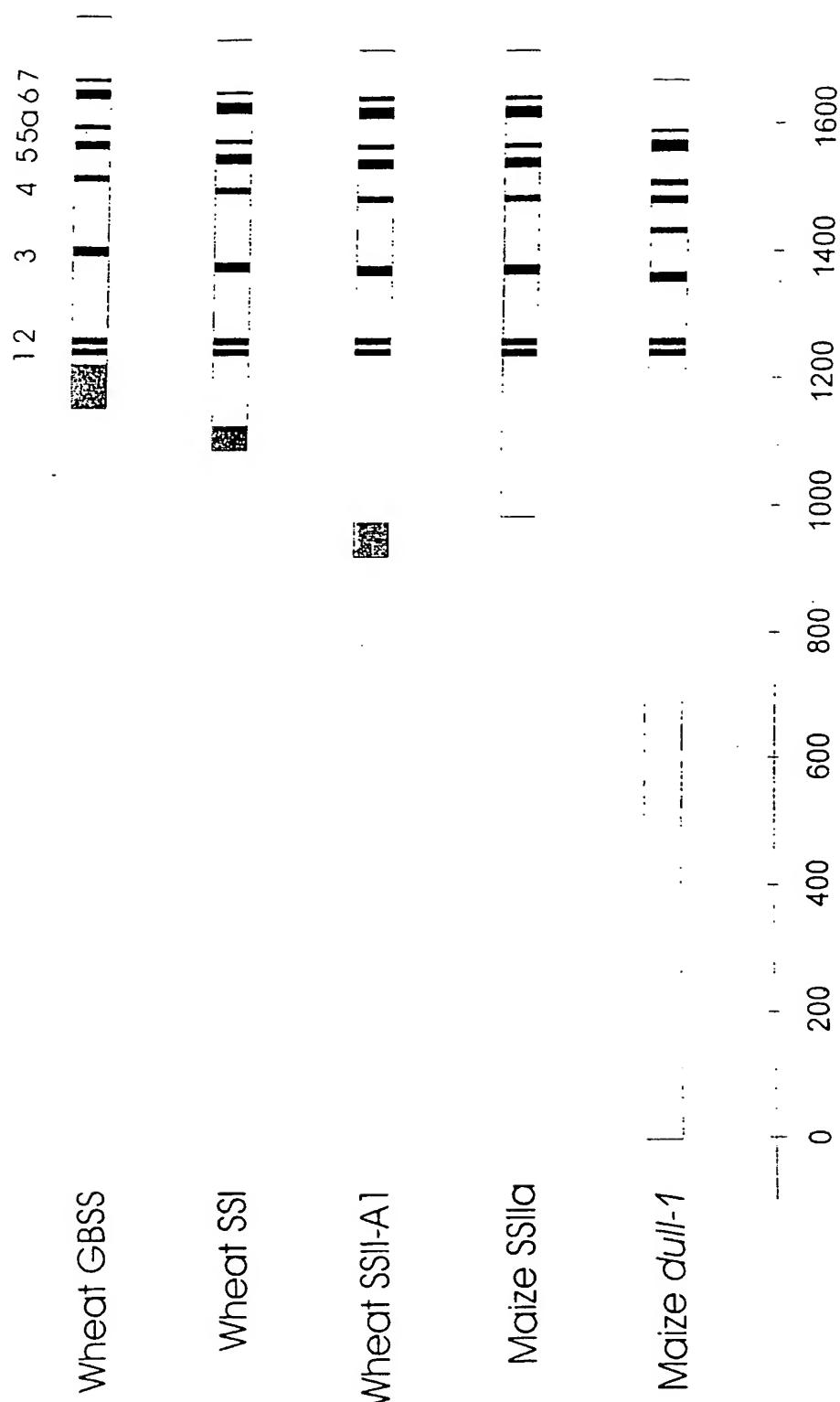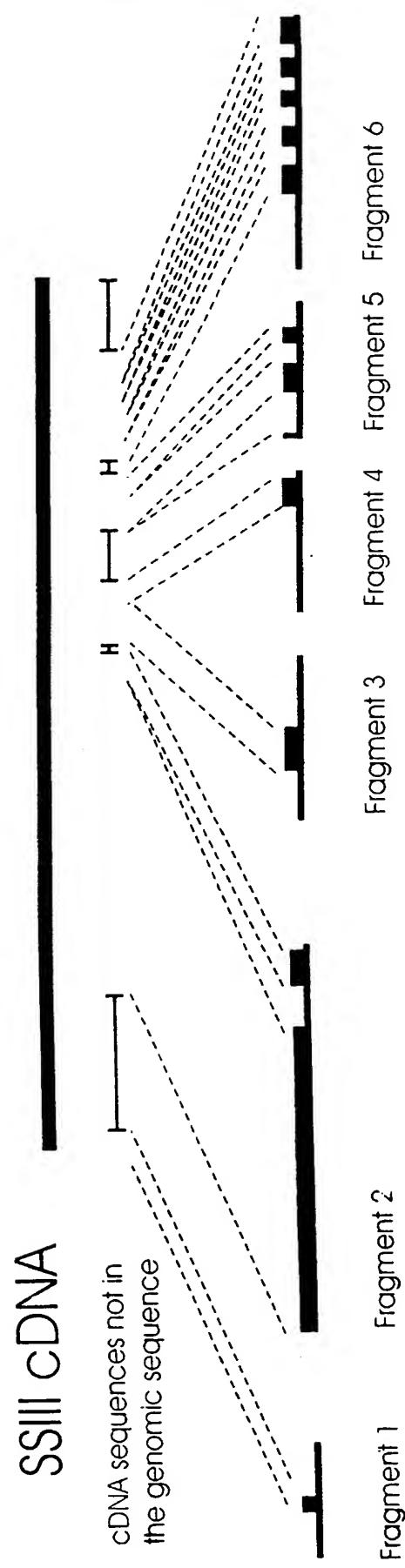
**FIGURE 10**
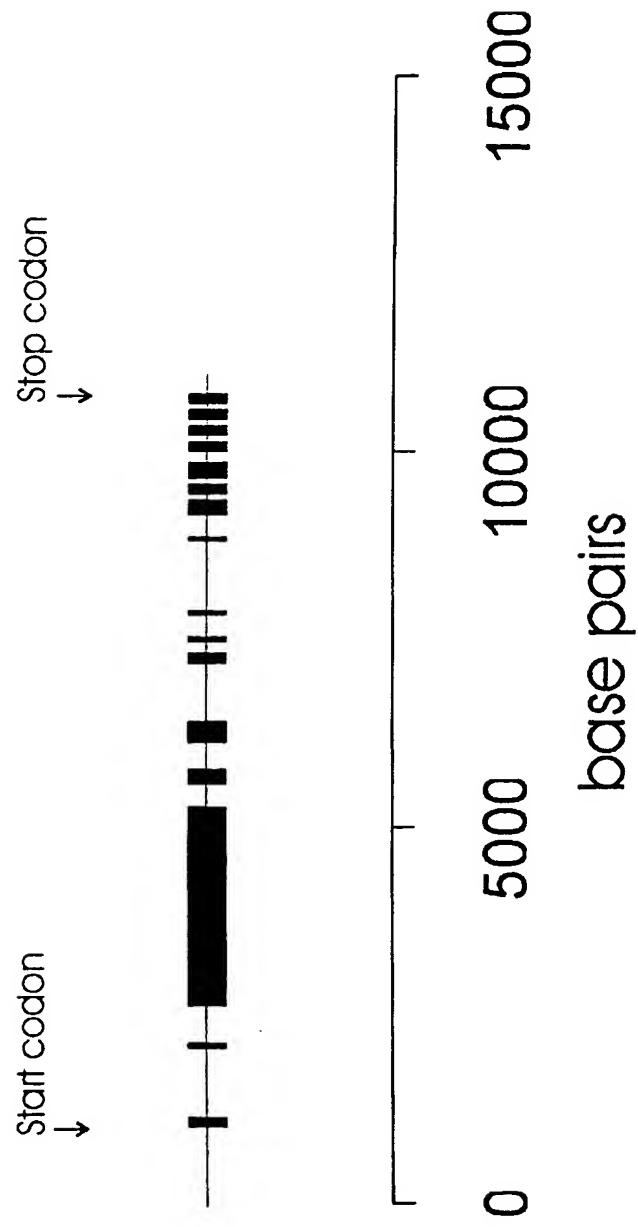
**FIGURE 11**

**FIGURE 12**

**FIGURE 13**

- 1 -

SEQUENCE LISTING

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      GOODMAN FIELDER LIMITED
      GROUPE LIMAGRAIN PACIFIC PTY LTD

<120> NOVEL GENES ENCODING WHEAT STARCH SYNTHASES AND USES
      THEREFOR

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<141> 2000-04-28

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gcggaccaac ccgcgcatcg tatcacgatc acccacccg atcccggccg ccgcc atg 178
                                                               Met
                                                               1

tcg tcg gcg gtc gcg tcc gcc gcg tcc ttc ctc gcg ctc gcg tcc gcc   226
Ser Ser Ala Val Ala Ser Ala Ala Ser Phe Leu Ala Leu Ala Ser Ala
            5                   10                  15

tcc ccc ggg aga tca cgg agg agg acg agg gtg agc gcg tcg cca ccc   274
Ser Pro Gly Arg Ser Arg Arg Arg Thr Arg Val Ser Ala Ser Pro Pro
        20                  25                  30

cac acc ggg gct ggc agg ttg cac tgg ccg ccg tcg ccg ccg cag cgc   322
His Thr Gly Ala Gly Arg Leu His Trp Pro Pro Ser Pro Pro Gln Arg
    35                  40                  45

acg gct cgc gac gga gcg gtg gcc gcg cgc gcc gcc ggg aag aag gac   370
Thr Ala Arg Asp Gly Ala Val Ala Ala Arg Ala Ala Gly Lys Lys Asp
50                  55                  60                  65

gcg ggg atc gac gac gcc gcg ccc gcg agg cag ccc cgc gca ctc cgc   418
Ala Gly Ile Asp Asp Ala Ala Pro Ala Arg Gln Pro Arg Ala Leu Arg
                70                  75                  80

ggt ggc gcc gcc acc aag gtt gcg gag cgg agg gat ccc gtc aag acg   466
Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val Lys Thr
            85                  90                  95

ctc gat cgc gac gcc gcg gaa ggt ggc gcg ccg tcc ccg ccg gca ccg   514
Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ser Pro Pro Ala Pro

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```
                100                    105                      110

agg cag gag gac gcc cgt ctg ccg agc atg aac ggc atg ccg gtg aac    562
Arg Gln Glu Asp Ala Arg Leu Pro Ser Met Asn Gly Met Pro Val Asn
    115             120                 125

ggt gaa aac aaa tct acc ggc ggc ggc ggc gcg act aaa gac agc ggg    610
Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp Ser Gly
130                 135                 140                 145

ctg ccc gca ccc gca cgc gcg ccc cag ccg tcg agc cag aac aga gta    658
Leu Pro Ala Pro Ala Arg Ala Pro Gln Pro Ser Ser Gln Asn Arg Val
                150                 155                 160

ccg gtg aat ggt gaa aac aaa gct aac gtc gcc tcg ccg ccg acg agc    706
Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro Thr Ser
                165                 170                 175

ata gcc gag gtc gcg gct ccg gat ccc gca gct acc att tcc atc agt    754
Ile Ala Glu Val Ala Ala Pro Asp Pro Ala Ala Thr Ile Ser Ile Ser
        180                 185                 190

gac aag gcg cca gag tcc gtt gtc cca gcc gag aag gcg ccg ccg tcg    802
Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Ala Pro Pro Ser
    195                 200                 205

tcc ggc tca aat ttc gtg ccc tcg gct tct gct ccc ggg tct gac act    850
Ser Gly Ser Asn Phe Val Pro Ser Ala Ser Ala Pro Gly Ser Asp Thr
210                 215                 220                 225

gtc agc gac gtg gaa ctt gaa ctg aag aag ggt gcg gtc att gtc aaa    898
Val Ser Asp Val Glu Leu Glu Leu Lys Lys Gly Ala Val Ile Val Lys
                230                 235                 240

gaa gct cca aac cca aag gct ctt tcg ccg ccc gca gca ccc gct gta    946
Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro Ala Val
                245                 250                 255

caa caa gac ctt tgg gac ttc aag aaa tac att ggt ttc gag gag ccc    994
Gln Gln Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu Glu Pro
        260                 265                 270

gtg gag gcc aag gat gat ggc cgg gct gtt gca gat gat gcg ggc tcc    1042
Val Glu Ala Lys Asp Asp Gly Arg Ala Val Ala Asp Asp Ala Gly Ser
    275                 280                 285

ttc gaa cac cac cag aat cac gat tcc ggg cct ttg gca ggg gag aac    1090
Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly Glu Asn
290                 295                 300                 305

gtc atg aac gtg gtc gtc gtg gct gct gaa tgt tct ccc tgg tgc aaa    1138
Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp Cys Lys
                310                 315                 320

aca ggt ggt ctt gga gat gtt gcc ggt gct ttg ccc aag gct ttg gcg    1186
Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala Leu Ala
                325                 330                 335

aag aga gga cat cgt gtt atg gtt gtg gta cca agg tat ggg gac tat    1234
Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly Asp Tyr
                340                 345                 350

gag gaa gcc tac gat gtc gga gtc cga aaa tac tac aag gct gct gga    1282
Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala Ala Gly
    355                 360                 365
```

- 3 -

```
cag gat atg gaa gtg aat tat ttc cat gct tat atc gat gga gtt gat    1330
Gln Asp Met Glu Val Asn Tyr Phe His Ala Tyr Ile Asp Gly Val Asp
370             375             380             385

ttt gtg ttc att gac gct cct ctc ttc cga cac cgc cag gaa gac att    1378
Phe Val Phe Ile Asp Ala Pro Leu Phe Arg His Arg Gln Glu Asp Ile
            390             395             400

tat ggg ggc agc aga cag gaa att atg aag cgc atg att ttg ttc tgc    1426
Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu Phe Cys
            405             410             415

aag gcc gct gtc gag gtt cca tgg cac gtt cca tgc ggc ggt gtc cct    1474
Lys Ala Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly Val Pro
            420             425             430

tat ggg gat gga aat ctg gtg ttt att gca aat gat tgg cac acg gca    1522
Tyr Gly Asp Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His Thr Ala
            435             440             445

ctc ctg cct gtc tat ctg aaa gca tat tac agg gac cat ggt ttg atg    1570
Leu Leu Pro Val Tyr Leu Lys Ala Tyr Tyr Arg Asp His Gly Leu Met
450             455             460             465

cag tac act cgg tcc att atg gtg ata cat aac atc gct cac cag ggc    1618
Gln Tyr Thr Arg Ser Ile Met Val Ile His Asn Ile Ala His Gln Gly
            470             475             480

cgt ggc cca gta gat gag ttc ccg ttc acc gag ttg cct gag cac tac    1666
Arg Gly Pro Val Asp Glu Phe Pro Phe Thr Glu Leu Pro Glu His Tyr
            485             490             495

ctg gaa cac ttc aga ctg tac gac ccc gtg ggt ggt gaa cac gcc aac    1714
Leu Glu His Phe Arg Leu Tyr Asp Pro Val Gly Gly Glu His Ala Asn
            500             505             510

tac ttc gcc gcc ggc ctg aag atg gcg gac cag gtt gtc gtc gtg agc    1762
Tyr Phe Ala Ala Gly Leu Lys Met Ala Asp Gln Val Val Val Val Ser
            515             520             525

ccg ggg tac ctg tgg gag ctg aag acg gtg gag ggc ggc tgg ggg ctt    1810
Pro Gly Tyr Leu Trp Glu Leu Lys Thr Val Glu Gly Gly Trp Gly Leu
530             535             540             545

cac gac atc ata cgg cag aac gac tgg aag acc cgc ggc atc gtg aac    1858
His Asp Ile Ile Arg Gln Asn Asp Trp Lys Thr Arg Gly Ile Val Asn
            550             555             560

ggc atc gac aac atg gag tgg aac ccc gag gtg gac gtc cac ctc aag    1906
Gly Ile Asp Asn Met Glu Trp Asn Pro Glu Val Asp Val His Leu Lys
            565             570             575

tcg gac ggc tac acc aac ttc tcc ctg ggg acg ctg gac tcc ggc aag    1954
Ser Asp Gly Tyr Thr Asn Phe Ser Leu Gly Thr Leu Asp Ser Gly Lys
            580             585             590

cgg cag tgc aag gag gcc ctg cag cgg gag ctg ggc ctg cag gtc cgc    2002
Arg Gln Cys Lys Glu Ala Leu Gln Arg Glu Leu Gly Leu Gln Val Arg
            595             600             605

ggc gac gtg ccg ctg ctc ggc ttc atc ggg cgc ctg gac ggg cag aag    2050
Gly Asp Val Pro Leu Leu Gly Phe Ile Gly Arg Leu Asp Gly Gln Lys
610             615             620             625
```

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```
ggc gtg gag atc atc gcg gac gcg atg ccc tgg atc gtg agc cag gac     2098
Gly Val Glu Ile Ile Ala Asp Ala Met Pro Trp Ile Val Ser Gln Asp
            630                 635                 640

gtg cag ctg gtc atg ctg ggc acc ggg cgc cac gac ctg gag ggc atg     2146
Val Gln Leu Val Met Leu Gly Thr Gly Arg His Asp Leu Glu Gly Met
            645                 650                 655

ctg cgg cac ttc gag cgg gag cac cac gac aag gtg cgc ggg tgg gtg     2194
Leu Arg His Phe Glu Arg Glu His His Asp Lys Val Arg Gly Trp Val
            660                 665                 670

ggg ttc tcc gtg cgg ctg gcg cac cgg atc acg gcc ggc gcc gac gcg     2242
Gly Phe Ser Val Arg Leu Ala His Arg Ile Thr Ala Gly Ala Asp Ala
            675                 680                 685

ctc ctc atg ccc tcc cgg ttc gag ccg tgc gga ctg aac cag ctc tac     2290
Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr
690                 695                 700                 705

gcc atg gcc tac ggc acc gtc ccc gtc gtg cat gcc gtc ggt ggc ctg     2338
Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly Leu
            710                 715                 720

agg gac acc gtg ccg ccg ttc gac ccc ttc aac cac tcc ggg ctc ggg     2386
Arg Asp Thr Val Pro Pro Phe Asp Pro Phe Asn His Ser Gly Leu Gly
            725                 730                 735

tgg acg ttc gac cgc gca gag gcg cag aag ctg atc gag gcg ctc ggg     2434
Trp Thr Phe Asp Arg Ala Glu Ala Gln Lys Leu Ile Glu Ala Leu Gly
            740                 745                 750

cac tgc ctc cgc acc tac cgg gac tac aag gag agc tgg agg ggg ctc     2482
His Cys Leu Arg Thr Tyr Arg Asp Tyr Lys Glu Ser Trp Arg Gly Leu
            755                 760                 765

cag gag cgc ggc atg tcg cag gac ttc agc tgg gag cat gcc gcc aag     2530
Gln Glu Arg Gly Met Ser Gln Asp Phe Ser Trp Glu His Ala Ala Lys
770                 775                 780                 785

ctc tac gag gac gtc ctc gtc aag gcc aag tac cag tgg tgaacgctag     2579
Leu Tyr Glu Asp Val Leu Val Lys Ala Lys Tyr Gln Trp
            790                 795

ctgctagccg gtccagcccc gcatgcgtgc atgacaggat ggaattgcgc attgcgcacg 2639

caggaaggtg ccatggagcg ccggcatccg cgaagtacag tgacatgagg tgtgtgtggt 2699

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tgttacaggt atatgggaat gttgttaact tggtattgta atttgttatg ttgtgtgcat 2819

tattacagag ggcaacgatc tgcgccggcg caccggccca actgttgggc cggtcgcaca 2879

gcagccgttg gatccgaccg cctgggccgt tggatcccac cgaaaaaaaa aaaaaaaaaa 2939
```

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<400> 2
Met Ser Ser Ala Val Ala Ser Ala Ala Ser Phe Leu Ala Leu Ala Ser
1               5                   10                  15
```

-5-

```
Ala Ser Pro Gly Arg Ser Arg Arg Arg Thr Arg Val Ser Ala Ser Pro
         20              25                  30

Pro His Thr Gly Ala Gly Arg Leu His Trp Pro Pro Ser Pro Pro Gln
         35              40              45

Arg Thr Ala Arg Asp Gly Ala Val Ala Ala Arg Ala Ala Gly Lys Lys
    50              55                  60

Asp Ala Gly Ile Asp Asp Ala Ala Pro Ala Arg Gln Pro Arg Ala Leu
65              70                  75                  80

Arg Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val Lys
                85                  90                  95

Thr Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ser Pro Pro Ala
         100             105                 110

Pro Arg Gln Glu Asp Ala Arg Leu Pro Ser Met Asn Gly Met Pro Val
         115             120                 125

Asn Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp Ser
    130             135                 140

Gly Leu Pro Ala Pro Ala Arg Ala Pro Gln Pro Ser Ser Gln Asn Arg
145             150                 155                 160

Val Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro Thr
             165             170                 175

Ser Ile Ala Glu Val Ala Ala Pro Asp Pro Ala Ala Thr Ile Ser Ile
         180             185                 190

Ser Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Ala Pro Pro
         195             200                 205

Ser Ser Gly Ser Asn Phe Val Pro Ser Ala Ser Ala Pro Gly Ser Asp
    210             215                 220

Thr Val Ser Asp Val Glu Leu Glu Leu Lys Lys Gly Ala Val Ile Val
225             230             235                 240

Lys Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro Ala
             245             250                 255

Val Gln Gln Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu Glu
             260             265                 270

Pro Val Glu Ala Lys Asp Asp Gly Arg Ala Val Ala Asp Asp Ala Gly
         275             280                 285

Ser Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly Glu
    290             295               . 300

Asn Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp Cys
305             310                 315                 320

Lys Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala Leu
         325             330                 335

Ala Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly Asp
         340             345                 350

Tyr Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala Ala
```

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```
         355                    360                    365

  Gly Gln Asp Met Glu Val Asn Tyr Phe His Ala Tyr Ile Asp Gly Val
      370                    375                380

  Asp Phe Val Phe Ile Asp Ala Pro Leu Phe Arg His Arg Gln Glu Asp
  385                    390                395                400

  Ile Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu Phe
                  405                410                415

  Cys Lys Ala Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly Val
                  420                425                430

  Pro Tyr Gly Asp Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His Thr
          435                440                445

  Ala Leu Leu Pro Val Tyr Leu Lys Ala Tyr Tyr Arg Asp His Gly Leu
      450                455                460

  Met Gln Tyr Thr Arg Ser Ile Met Val Ile His Asn Ile Ala His Gln
  465                    470                475                480

  Gly Arg Gly Pro Val Asp Glu Phe Pro Phe Thr Glu Leu Pro Glu His
                  485                490                495

  Tyr Leu Glu His Phe Arg Leu Tyr Asp Pro Val Gly Gly Glu His Ala
              500                505                510

  Asn Tyr Phe Ala Ala Gly Leu Lys Met Ala Asp Gln Val Val Val Val
              515                520                525

  Ser Pro Gly Tyr Leu Trp Glu Leu Lys Thr Val Glu Gly Gly Trp Gly
      530                535                540

  Leu His Asp Ile Ile Arg Gln Asn Asp Trp Lys Thr Arg Gly Ile Val
  545                    550                555                560

  Asn Gly Ile Asp Asn Met Glu Trp Asn Pro Glu Val Asp Val His Leu
                  565                570                575

  Lys Ser Asp Gly Tyr Thr Asn Phe Ser Leu Gly Thr Leu Asp Ser Gly
              580                585                590

  Lys Arg Gln Cys Lys Glu Ala Leu Gln Arg Glu Leu Gly Leu Gln Val
          595                600                605

  Arg Gly Asp Va' Pro Leu Leu Gly Phe Ile Gly Arg Leu Asp Gly Gln
      610                615                620

  Lys Gly Val Glu Ile Ile Ala Asp Ala Met Pro Trp Ile Val Ser Gln
  625                    630                635                640

  Asp Val Gln Leu Val Met Leu Gly Thr Gly Arg His Asp Leu Glu Gly
                  645                650                655

  Met Leu Arg His Phe Glu Arg Glu His His Asp Lys Val Arg Gly Trp
              660                665                670

  Val Gly Phe Ser Val Arg Leu Ala His Arg Ile Thr Ala Gly Ala Asp
          675                680                685

  Ala Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu
      690                695                700
```

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```
Tyr Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly
705             710             715             720

Leu Arg Asp Thr Val Pro Pro Phe Asp Pro Phe Asn His Ser Gly Leu
            725             730             735

Gly Trp Thr Phe Asp Arg Ala Glu Ala Gln Lys Leu Ile Glu Ala Leu
            740             745             750

Gly His Cys Leu Arg Thr Tyr Arg Asp Tyr Lys Glu Ser Trp Arg Gly
        755             760             765

Leu Gln Glu Arg Gly Met Ser Gln Asp Phe Ser Trp Glu His Ala Ala
    770             775             780

Lys Leu Tyr Glu Asp Val Leu Val Lys Ala Lys Tyr Gln Trp
785             790             795
```

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atcgcccgcc ccgatcccgg ccgccgcc atg tcg tcg gcg gtc gcg tcc gcc     112
                                Met Ser Ser Ala Val Ala Ser Ala
                                 1               5

gcg tcc ttc ctc gcg ctc gcc tcc gcc tcc ccc ggg aga tca cgc agg   160
Ala Ser Phe Leu Ala Leu Ala Ser Ala Ser Pro Gly Arg Ser Arg Arg
     10              15              20

cgg gcg agg gtg agc gcg ccg cca ccc cac gcc ggg gcc ggc agg ctg   208
Arg Ala Arg Val Ser Ala Pro Pro Pro His Ala Gly Ala Gly Arg Leu
25              30              35              40

cac tgg ccg ccg tgg ccg ccg cag cgc acg gct cgc gac gga ggt gtg   256
His Trp Pro Pro Trp Pro Pro Gln Arg Thr Ala Arg Asp Gly Gly Val
            45              50              55

gcc gcg cgc gcc gcc ggg aag aag gac gcg agg gtc gac gac gac gcc   304
Ala Ala Arg Ala Ala Gly Lys Lys Asp Ala Arg Val Asp Asp Asp Ala
        60              65              70

gcg tcc gcg agg cag ccc cgc gca cgc cgc ggt ggc gcc gcc acc aag   352
Ala Ser Ala Arg Gln Pro Arg Ala Arg Arg Gly Gly Ala Ala Thr Lys
        75              80              85

gtc gcg gag cgg agg gat ccc gtc aag acg ctc gat cgc gac gcc gcg   400
Val Ala Glu Arg Arg Asp Pro Val Lys Thr Leu Asp Arg Asp Ala Ala
    90              95              100

gaa ggt ggc gcg ccg gca ccg ccg gca ccg agg cag gac gcc gcc cgt   448
Glu Gly Gly Ala Pro Ala Pro Pro Ala Pro Arg Gln Asp Ala Ala Arg
105             110             115             120

cca ccg agt atg aac ggc acg ccg gtg aac ggt gag aac aaa tct acc   496
Pro Pro Ser Met Asn Gly Thr Pro Val Asn Gly Glu Asn Lys Ser Thr
```

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```
                    125                      130                      135

ggc ggc ggc ggc gcg acc aaa gac agc ggg ctg ccc gca ccc gca cgc    544
Gly Gly Gly Gly Ala Thr Lys Asp Ser Gly Leu Pro Ala Pro Ala Arg
            140                  145                  150

gcg ccc cat ccg tcg acc cag aac aga gta cca gtg aac ggt gaa aac    592
Ala Pro His Pro Ser Thr Gln Asn Arg Val Pro Val Asn Gly Glu Asn
        155                  160                  165

aaa gct aac gtc gcc tcg ccg ccg acg agc ata gcc gag gtc gtg gct    640
Lys Ala Asn Val Ala Ser Pro Pro Thr Ser Ile Ala Glu Val Val Ala
    170                  175                  180

ccg gat tcc gca gct acc att tcc atc agt gac aag gcg ccg gag tcc    688
Pro Asp Ser Ala Ala Thr Ile Ser Ile Ser Asp Lys Ala Pro Glu Ser
185                  190                  195                  200

gtt gtc cca gcc gag aag ccg ccg ccg tcg tcc ggc tca aat ttc gtg    736
Val Val Pro Ala Glu Lys Pro Pro Pro Ser Ser Gly Ser Asn Phe Val
                    205                  210                  215

gtc tcg gct tct gct ccc agg ctg gac att gac agc gat gtt gaa cct    784
Val Ser Ala Ser Ala Pro Arg Leu Asp Ile Asp Ser Asp Val Glu Pro
            220                  225                  230

gaa ctg aag aag ggt gcg gtc atc gtc gaa gaa gct cca aac cca aag    832
Glu Leu Lys Lys Gly Ala Val Ile Val Glu Glu Ala Pro Asn Pro Lys
        235                  240                  245

gct ctt tcg ccg cct gca gcc ccc gct gta caa gaa gac ctt tgg gac    880
Ala Leu Ser Pro Pro Ala Ala Pro Ala Val Gln Glu Asp Leu Trp Asp
    250                  255                  260

ttc aag aaa tac att ggc ttc gag gag ccc gtg gag gcc aag gat gat    928
Phe Lys Lys Tyr Ile Gly Phe Glu Glu Pro Val Glu Ala Lys Asp Asp
265                  270                  275                  280

ggc tgg gct gtt gca gat gat gcg ggc tcc ttt gaa cat cac cag aac    976
Gly Trp Ala Val Ala Asp Asp Ala Gly Ser Phe Glu His His Gln Asn
            285                  290                  295

cat gat tcc gga cct ttg gca ggg gag aac gtc atg aac gtg gtc gtc   1024
His Asp Ser Gly Pro Leu Ala Gly Glu Asn Val Met Asn Val Val Val
        300                  305                  310

gtg gct gct gaa tgt tct ccc tgg tgc aaa aca ggt ggt ctt gga gat   1072
Val Ala Ala Glu Cys Ser Pro Trp Cys Lys Thr Gly Gly Leu Gly Asp
        315                  320                  325

gtt gcc ggt gct ttg ccc aag gct ttg gcg aag aga gga cat cgt gtt   1120
Val Ala Gly Ala Leu Pro Lys Ala Leu Ala Lys Arg Gly His Arg Val
    330                  335                  340

atg gtt gtg gta cca agg tat ggg gac tat gag gaa gcc tac gat gtc   1168
Met Val Val Val Pro Arg Tyr Gly Asp Tyr Glu Glu Ala Tyr Asp Val
345                  350                  355                  360

gga gtc cga aaa tac tac aag gct gct gga cag gat atg gaa gtg aat   1216
Gly Val Arg Lys Tyr Tyr Lys Ala Ala Gly Gln Asp Met Glu Val Asn
            365                  370                  375

tat ttc cat gct tat atc gat gga gtt gat ttt gtg ttc att gac gct   1264
Tyr Phe His Ala Tyr Ile Asp Gly Val Asp Phe Val Phe Ile Asp Ala
            380                  385                  390
```

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cct ctc ttc cga cac cgc cag gaa gac att tat ggg ggc agc aga cag      1312
Pro Leu Phe Arg His Arg Gln Glu Asp Ile Tyr Gly Gly Ser Arg Gln
        395                 400                 405

gaa att atg aag cgc atg att ttg ttc tgc aag gcc gct gtc gag gtt      1360
Glu Ile Met Lys Arg Met Ile Leu Phe Cys Lys Ala Ala Val Glu Val
        410                 415                 420

cct tgg cac gtt cca tgc ggc ggt gtc cct tat ggg gat gga aat ctg      1408
Pro Trp His Val Pro Cys Gly Gly Val Pro Tyr Gly Asp Gly Asn Leu
425                 430                 435                 440

gtg ttt att gca aat gat tgg cac acg gca ctc ctg cct gtc tat ctg      1456
Val Phe Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro Val Tyr Leu
                445                 450                 455

aaa gca tat tac agg gac cat ggt ttg atg cag tac act cgg tcc att      1504
Lys Ala Tyr Tyr Arg Asp His Gly Leu Met Gln Tyr Thr Arg Ser Ile
                460                 465                 470

atg gtg ata cat aac atc gcg cac cag ggc cgt ggc cca gta gat gaa      1552
Met Val Ile His Asn Ile Ala His Gln Gly Arg Gly Pro Val Asp Glu
            475                 480                 485

ttc ccg ttc acc gag ttg cct gag cac tac ctg gaa cac ttc aga ctg      1600
Phe Pro Phe Thr Glu Leu Pro Glu His Tyr Leu Glu His Phe Arg Leu
        490                 495                 500

tac gac ccc gtg ggt ggt gag cac gcc aac tac ttc gcc gcc ggc ctg      1648
Tyr Asp Pro Val Gly Gly Glu His Ala Asn Tyr Phe Ala Ala Gly Leu
505                 510                 515                 520

aag atg gcg gac cag gtt gtc gtg gtg agc ccc ggg tac ctg tgg gag      1696
Lys Met Ala Asp Gln Val Val Val Val Ser Pro Gly Tyr Leu Trp Glu
                525                 530                 535

ctc aag acg gtg gag ggc ggc tgg ggg ctt cac gac atc ata cgg cag      1744
Leu Lys Thr Val Glu Gly Gly Trp Gly Leu His Asp Ile Ile Arg Gln
                540                 545                 550

aac gac tgg aag acc cgc ggc atc gtc aac ggc atc gac aac atg gag      1792
Asn Asp Trp Lys Thr Arg Gly Ile Val Asn Gly Ile Asp Asn Met Glu
                555                 560                 565

tgg aac ccc gag gtg gac gtc cac ctc aag tcg gac ggc tac acc aac      1840
Trp Asn Pro Glu Val Asp Val His Leu Lys Ser Asp Gly Tyr Thr Asn
        570                 575                 580

ttc tcc ctg ggg acg ctg gac tcc ggc aag cgg cag tgc aag gag gcc      1888
Phe Ser Leu Gly Thr Leu Asp Ser Gly Lys Arg Gln Cys Lys Glu Ala
585                 590                 595                 600

ctg cag cgc gag ctg ggc ctg cag gtc cgc gcc gac gtg ccg ctg ctc      1936
Leu Gln Arg Glu Leu Gly Leu Gln Val Arg Ala Asp Val Pro Leu Leu
                605                 610                 615

ggc ttc atc ggc cgc ctg gac ggg cag aag ggc gtg gag atc atc gcg      1984
Gly Phe Ile Gly Arg Leu Asp Gly Gln Lys Gly Val Glu Ile Ile Ala
                620                 625                 630

gac gcc atg ccc tgg atc gtg agc cag gac gtg cag ctg gtc atg ctg      2032
Asp Ala Met Pro Trp Ile Val Ser Gln Asp Val Gln Leu Val Met Leu
                635                 640                 645
```

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```
ggc acc ggc cgc cac gac ctg gag agc atg ctg cgg cac ttc gag cgg    2080
Gly Thr Gly Arg His Asp Leu Glu Ser Met Leu Arg His Phe Glu Arg
    650             655             660

gag cac cac gac aag gtg cgc ggg tgg gtg ggg ttc tcc gtg cgc ctg    2128
Glu His His Asp Lys Val Arg Gly Trp Val Gly Phe Ser Val Arg Leu
665             670             675             680

gcg cac cgg atc acg gcg ggc gcc gac gcg ctc ctc atg ccc tcc cgg    2176
Ala His Arg Ile Thr Ala Gly Ala Asp Ala Leu Leu Met Pro Ser Arg
                685             690             695

ttc gag ccg tgc ggg ttg aac cag ctt tac gcc atg gcc tac ggc acc    2224
Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala Tyr Gly Thr
            700             705             710

gtc ccc gtc gtg cac gcc gtc ggc ggg gtg agg gac acc gtg ccg ccg    2272
Val Pro Val Val His Ala Val Gly Gly Val Arg Asp Thr Val Pro Pro
            715             720             725

ttc gac ccc ttc aac cac tcc ggc ctc ggg tgg acg ttc gac cgc gcc    2320
Phe Asp Pro Phe Asn His Ser Gly Leu Gly Trp Thr Phe Asp Arg Ala
    730             735             740

gag gcg cac aag ctg atc gag gcg ctc ggg cac tgc ctc cgc acc tac    2368
Glu Ala His Lys Leu Ile Glu Ala Leu Gly His Cys Leu Arg Thr Tyr
745             750             755             760

cgg gac tac aag gag agc tgg agg ggc ctc cag gag cgc ggc atg tcg    2416
Arg Asp Tyr Lys Glu Ser Trp Arg Gly Leu Gln Glu Arg Gly Met Ser
                765             770             775

cag gac ttc agc tgg gag cat gcc gcc aag ctc tac gag gac gtc ctc    2464
Gln Asp Phe Ser Trp Glu His Ala Ala Lys Leu Tyr Glu Asp Val Leu
            780             785             790

ctc aag gcc aag tac cag tgg tgaacgctag ctgctagccg ctccagcccc    2515
Leu Lys Ala Lys Tyr Gln Trp
            795

gcatgcgtgc atgcatgaga gggtggaact gcgcattgcg cccgcaggaa cgtgccatcc 2575

ttctcgatgg gagcgccggc atccgcgagg tgcagtgaca tgagaggtgt gtgtggttga 2635

gacgctgatt ccgatctcga tctggtccgt agcagagtag agcggacgta gggaagcgct 2695

ccttgttgca ggtatatggg aatgttgtca acttggtatt gtagtttgct atgttgtatg 2755

cgttattaca atgttgttac ttattcttgt taagtcggag gcaaagggcg aaagctagct 2815

cacatgaaaa aaaaaaaaaa aaaaaaa                                      2842
```

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<210> 4
<211> 799
<212> PRT
<213> Triticum aestivum

<400> 4
Met Ser Ser Ala Val Ala Ser Ala Ala Ser Phe Leu Ala Leu Ala Ser
1               5               10              15

Ala Ser Pro Gly Arg Ser Arg Arg Arg Ala Arg Val Ser Ala Pro Pro
            20              25              30
```

```
Pro His Ala Gly Ala Gly Arg Leu His Trp Pro Pro Trp Pro Pro Gln
        35              40              45

Arg Thr Ala Arg Asp Gly Gly Val Ala Ala Arg Ala Ala Gly Lys Lys
        50              55              60

Asp Ala Arg Val Asp Asp Asp Ala Ala Ser Ala Arg Gln Pro Arg Ala
65              70              75              80

Arg Arg Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val
                85              90              95

Lys Thr Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ala Pro Pro
            100             105             110

Ala Pro Arg Gln Asp Ala Ala Arg Pro Pro Ser Met Asn Gly Thr Pro
        115             120             125

Val Asn Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp
    130             135             140

Ser Gly Leu Pro Ala Pro Ala Arg Ala Pro His Pro Ser Thr Gln Asn
145             150             155             160

Arg Val Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro
            165             170             175

Thr Ser Ile Ala Glu Val Val Ala Pro Asp Ser Ala Ala Thr Ile Ser
            180             185             190

Ile Ser Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Pro Pro
        195             200             205

Pro Ser Ser Gly Ser Asn Phe Val Val Ser Ala Ser Ala Pro Arg Leu
    210             215             220

Asp Ile Asp Ser Asp Val Glu Pro Glu Leu Lys Lys Gly Ala Val Ile
225             230             235             240

Val Glu Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro
            245             250             255

Ala Val Gln Glu Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu
            260             265             270

Glu Pro Val Glu Ala Lys Asp Asp Gly Trp Ala Val Ala Asp Asp Ala
        275             280             285

Gly Ser Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly
    290             295             300

Glu Asn Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp
305             310             315             320

Cys Lys Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala
            325             330             335

Leu Ala Lys Arg Gly His Arg Val Met Val Val Pro Arg Tyr Gly
        340             345             350

Asp Tyr Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala
    355             360             365

Ala Gly Gln Asp Met Glu Val Asn Tyr Phe His Ala Tyr Ile Asp Gly
370             375             380
```

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```
Val Asp Phe Val Phe Ile Asp Ala Pro Leu Phe Arg His Arg Gln Glu
385             390             395             400

Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu
            405             410             415

Phe Cys Lys Ala Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly
        420             425             430

Val Pro Tyr Gly Asp Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His
        435             440             445

Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala Tyr Tyr Arg Asp His Gly
    450             455             460

Leu Met Gln Tyr Thr Arg Ser Ile Met Val Ile His Asn Ile Ala His
465             470             475             480

Gln Gly Arg Gly Pro Val Asp Glu Phe Pro Phe Thr Glu Leu Pro Glu
            485             490             495

His Tyr Leu Glu His Phe Arg Leu Tyr Asp Pro Val Gly Gly Glu His
        500             505             510

Ala Asn Tyr Phe Ala Ala Gly Leu Lys Met Ala Asp Gln Val Val Val
        515             520             525

Val Ser Pro Gly Tyr Leu Trp Glu Leu Lys Thr Val Glu Gly Gly Trp
    530             535             540

Gly Leu His Asp Ile Ile Arg Gln Asn Asp Trp Lys Thr Arg Gly Ile
545             550             555             560

Val Asn Gly Ile Asp Asn Met Glu Trp Asn Pro Glu Val Asp Val His
            565             570             575

Leu Lys Ser Asp Gly Tyr Thr Asn Phe Ser Leu Gly Thr Leu Asp Ser
            580             585             590

Gly Lys Arg Gln Cys Lys Glu Ala Leu Gln Arg Glu Leu Gly Leu Gln
        595             600             605

Val Arg Ala Asp Val Pro Leu Leu Gly Phe Ile Gly Arg Leu Asp Gly
    610             615             620

Gln Lys Gly Val Glu Ile Ile Ala Asp Ala Met Pro Trp Ile Val Ser
625             630             635             640

Gln Asp Val Gln Leu Val Met Leu Gly Thr Gly Arg His Asp Leu Glu
            645             650             655

Ser Met Leu Arg His Phe Glu Arg Glu His His Asp Lys Val Arg Gly
            660             665             670

Trp Val Gly Phe Ser Val Arg Leu Ala His Arg Ile Thr Ala Gly Ala
        675             680             685

Asp Ala Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln
        690             695             700

Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly
705             710             715             720

Gly Val Arg Asp Thr Val Pro Pro Phe Asp Pro Phe Asn His Ser Gly
```

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```
                 725                    730                    735
    Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala His Lys Leu Ile Glu Ala
                 740                    745                    750

    Leu Gly His Cys Leu Arg Thr Tyr Arg Asp Tyr Lys Glu Ser Trp Arg
                 755                    760                    765

    Gly Leu Gln Glu Arg Gly Met Ser Gln Asp Phe Ser Trp Glu His Ala
         770                    775                    780

    Ala Lys Leu Tyr Glu Asp Val Leu Leu Lys Ala Lys Tyr Gln Trp
    785                    790                    795
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<210> 5
<211> 2107
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(1791)

<400> 5

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cca gct gag aag acg ccg ccg tcg tcc ggc tca aat ttc gag tcc tcg       48
Pro Ala Glu Lys Thr Pro Pro Ser Ser Gly Ser Asn Phe Glu Ser Ser
 1               5                   10                  15

gcc tct gct ccc ggg tct gac act gtc agc gac gtg gaa caa gaa ctg       96
Ala Ser Ala Pro Gly Ser Asp Thr Val Ser Asp Val Glu Gln Glu Leu
                20                  25                  30

aag aag ggt gcg gtc gtt gtc gaa gaa gct cca aag cca aag gct ctt      144
Lys Lys Gly Ala Val Val Val Glu Glu Ala Pro Lys Pro Lys Ala Leu
            35                  40                  45

tcg ccg cct gca gcc ccc gct gta caa gaa gac ctt tgg gat ttc aag      192
Ser Pro Pro Ala Ala Pro Ala Val Gln Glu Asp Leu Trp Asp Phe Lys
        50                  55                  60

aaa tac att ggt ttc gag gag ccc gtg gag gcc aag gat gat ggc cgg      240
Lys Tyr Ile Gly Phe Glu Glu Pro Val Glu Ala Lys Asp Asp Gly Arg
 65                  70                  75                  80

gct gtc gca gat gat gcg ggc tcc ttt gaa cac cac cag aat cac gac      288
Ala Val Ala Asp Asp Ala Gly Ser Phe Glu His His Gln Asn His Asp
                85                  90                  95

tcc gga cct ttg gca ggg gag aat gtc atg aac gtg gtc gtc gtg gct      336
Ser Gly Pro Leu Ala Gly Glu Asn Val Met Asn Val Val Val Val Ala
            100                 105                 110

gct gag tgt tct ccc tgg tgc aaa aca ggt ggt ctg gga gat gtt gcg      384
Ala Glu Cys Ser Pro Trp Cys Lys Thr Gly Gly Leu Gly Asp Val Ala
            115                 120                 125

ggt gct ctg ccc aag gct ttg gca aag aga gga cat cgt gtt atg gtt      432
Gly Ala Leu Pro Lys Ala Leu Ala Lys Arg Gly His Arg Val Met Val
        130                 135                 140

gtg gta cca agg tat ggg gac tat gaa gaa cct acg gat gtc gga gtc      480
Val Val Pro Arg Tyr Gly Asp Tyr Glu Glu Pro Thr Asp Val Gly Val
145                 150                 155                 160
```

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```
cga aaa tac tac aag gct gct gga cag gat atg gaa gtg aat tat ttc    528
Arg Lys Tyr Tyr Lys Ala Ala Gly Gln Asp Met Glu Val Asn Tyr Phe
            165             170             175

cat gct tat atc gat gga gtt gat ttt gtg ttc att gac gct cct ctc    576
His Ala Tyr Ile Asp Gly Val Asp Phe Val Phe Ile Asp Ala Pro Leu
            180             185      .          190

ttc cga cac cga gag gaa gac att tat ggg ggc agc aga cag gaa att    624
Phe Arg His Arg Glu Glu Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile
            195             200             205

atg aag cgc atg att ttg ttc tgc aag gcc gct gtt gag gtt cca tgg    672
Met Lys Arg Met Ile Leu Phe Cys Lys Ala Ala Val Glu Val Pro Trp
    210             215             220

cac gtt cca tgc ggc ggt gtc cct tat ggg gat gga aat ctg gtg ttt    720
His Val Pro Cys Gly Gly Val Pro Tyr Gly Asp Gly Asn Leu Val Phe
225             230             235             240

att gca aat gat tgg cac acg gca ctc ctg cct gtc tat ctg aaa gca    768
Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala
            245             250             255

tat tac agg gac cat ggt ttg atg cag tac act cgg tcc att atg gtg    816
Tyr Tyr Arg Asp His Gly Leu Met Gln Tyr Thr Arg Ser Ile Met Val
            260             265             270

ata cat aac atc gct cac cag ggc cgt ggc cct gta gat gaa ttc ccg    864
Ile His Asn Ile Ala His Gln Gly Arg Gly Pro Val Asp Glu Phe Pro
            275             280             285

ttc acc gag ttg cct gag cac tac ctg gaa cac ttc aga ctg tac gac    912
Phe Thr Glu Leu Pro Glu His Tyr Leu Glu His Phe Arg Leu Tyr Asp
    290             295             300

ccc gtg ggt ggt gaa cac gcc aac tac ttc gcc gcc ggc ctg aag atg    960
Pro Val Gly Gly Glu His Ala Asn Tyr Phe Ala Ala Gly Leu Lys Met
305             310             315             320

gcg gac cag gtt gtc gtg gtg agc ccc ggg tac ctg tgg gag ctg aag   1008
Ala Asp Gln Val Val Val Val Ser Pro Gly Tyr Leu Trp Glu Leu Lys
            325             330             335                   .

acg gtg gag ggc ggc tgg ggg ctt cac gac atc ata cgg cag aac gac   1056
Thr Val Glu Gly Gly Trp Gly Leu His Asp Ile Ile Arg Gln Asn Asp
            340             345             350

tgg aag acc cgc ggc atc gtc aac ggc atc gac aac atg gag tgg aac   1104
Trp Lys Thr Arg Gly Ile Val Asn Gly Ile Asp Asn Met Glu Trp Asn
            355             360             365

ccc gag gtg gac gcc cac ctc aag tcg gac ggc tac acc aac ttc tcc   1152
Pro Glu Val Asp Ala His Leu Lys Ser Asp Gly Tyr Thr Asn Phe Ser
    370             375             380

ctg agg acg ctg gac tcc ggc aag cgg cag tgc aag gag gcc ctg cag   1200
Leu Arg Thr Leu Asp Ser Gly Lys Arg Gln Cys Lys Glu Ala Leu Gln
385             390             395             400

cgc gag ctg ggc ctg cag gtc cgc gcc gac gtg ccg ctg ctc ggc ttc   1248
Arg Glu Leu Gly Leu Gln Val Arg Ala Asp Val Pro Leu Leu Gly Phe
            405             410             415

atc ggc cgc ctg gac ggg cag aag ggc gtg gag atc atc gcg gac gcc   1296
```

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```
            Ile Gly Arg Leu Asp Gly Gln Lys Gly Val Glu Ile Ile Ala Asp Ala
                          420             425             430

atg ccc tgg atc gtg agc cag gac gtg cag ctg gtg atg ctg ggc acc          1344
Met Pro Trp Ile Val Ser Gln Asp Val Gln Leu Val Met Leu Gly Thr
            435             440             445

ggg cgc cac gac ctg gag agc atg ctg cag cac ttc gag cgg gag cac          1392
Gly Arg His Asp Leu Glu Ser Met Leu Gln His Phe Glu Arg Glu His
    450             455             460

cac gac aag gtg cgc ggg tgg gtg ggg ttc tcc gtg cgc ctg gcg cac          1440
His Asp Lys Val Arg Gly Trp Val Gly Phe Ser Val Arg Leu Ala His
465             470             475             480

cgg atc acg gcg ggg gcg gac gcg ctc ctc atg ccc tcc cgg ttc gtg          1488
Arg Ile Thr Ala Gly Ala Asp Ala Leu Leu Met Pro Ser Arg Phe Val
                485             490             495

ccg tgc ggg ctg aac cag ctc tac gcc atg gcc tac ggc acc gtc ccc          1536
Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro
            500             505             510

gtc gtg cac gcc gtc ggc ggc ctc agg gac acc gtg ccg ccg ttc gac          1584
Val Val His Ala Val Gly Gly Leu Arg Asp Thr Val Pro Pro Phe Asp
            515             520             525

ccc ttc aac cac tcc ggg ctc ggg tgg acg ttc gac cgc gcc gag gcg          1632
Pro Phe Asn His Ser Gly Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala
    530             535             540

cac aag ctg atc gag gcg ctc ggg cac tgc ctc cgc acc tac cga gac          1680
His Lys Leu Ile Glu Ala Leu Gly His Cys Leu Arg Thr Tyr Arg Asp
545             550             555             560

ttc aag gag agc tgg agg gcc ctc cag gag cgc ggc atg tcg cag gac          1728
Phe Lys Glu Ser Trp Arg Ala Leu Gln Glu Arg Gly Met Ser Gln Asp
                565             570             575

ttc agc tgg gag cac gcc gcc aag ctc tac gag gac gtc ctc gtc aag          1776
Phe Ser Trp Glu His Ala Ala Lys Leu Tyr Glu Asp Val Leu Val Lys
            580             585             590

gcc aag tac cag tgg tgaacgctag ctgctagccg ctccagcccc gcatgcgtgc          1831
Ala Lys Tyr Gln Trp
            595

atgacaggat ggaactgcat tgcgcacgca ggaaagtgcc atggagcgcc ggcatccgcg          1891

aagtacagtg acatgaggtg tgtgtggttg agacgctgat tccaatccgg cccgtagcag          1951

agtagagcgg aggtatatgg gaatcttaac ttggtattgt aatttgttat gttgtgtgca          2011

ttattacaat gttgttactt attcttgtta agtcggaggc caagggcgaa agctagctca          2071

catgtctgat ggatgcaaaa aaaaaaaaaa aaaaa                   .                    2107
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<210> 6
<211> 597
<212> PRT
<213> Triticum aestivum

<400> 6
Pro Ala Glu Lys Thr Pro Pro Ser Ser Gly Ser Asn Phe Glu Ser Ser

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1                    5                    10                   15

Ala Ser Ala Pro Gly Ser Asp Thr Val Ser Asp Val Glu Gln Glu Leu
                20                  25                  30

Lys Lys Gly Ala Val Val Val Glu Glu Ala Pro Lys Pro Lys Ala Leu
            35                  40                  45

Ser Pro Pro Ala Ala Pro Ala Val Gln Glu Asp Leu Trp Asp Phe Lys
    50                  55                  60

Lys Tyr Ile Gly Phe Glu Glu Pro Val Glu Ala Lys Asp Asp Gly Arg
65                  70                  75                  80

Ala Val Ala Asp Asp Ala Gly Ser Phe Glu His His Gln Asn His Asp
                85                  90                  95

Ser Gly Pro Leu Ala Gly Glu Asn Val Met Asn Val Val Val Val Ala
            100                 105                 110

Ala Glu Cys Ser Pro Trp Cys Lys Thr Gly Gly Leu Gly Asp Val Ala
        115                 120                 125

Gly Ala Leu Pro Lys Ala Leu Ala Lys Arg Gly His Arg Val Met Val
    130                 135                 140

Val Val Pro Arg Tyr Gly Asp Tyr Glu Glu Pro Thr Asp Val Gly Val
145                 150                 155                 160

Arg Lys Tyr Tyr Lys Ala Ala Gly Gln Asp Met Glu Val Asn Tyr Phe
                165                 170                 175

His Ala Tyr Ile Asp Gly Val Asp Phe Val Phe Ile Asp Ala Pro Leu
            180                 185                 190

Phe Arg His Arg Glu Glu Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile
    195                 200                 205

Met Lys Arg Met Ile Leu Phe Cys Lys Ala Ala Val Glu Val Pro Trp
210                 215                 220

His Val Pro Cys Gly Gly Val Pro Tyr Gly Asp Gly Asn Leu Val Phe
225                 230                 235                 240

Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala
            245                 250                 255

Tyr Tyr Arg Asp His Gly Leu Met Gln Tyr Thr Arg Ser Ile Met Val
            260                 265                 270

Ile His Asn Ile Ala His Gln Gly Arg Gly Pro Val Asp Glu Phe Pro
        275                 280                 285

Phe Thr Glu Leu Pro Glu His Tyr Leu Glu His Phe Arg Leu Tyr Asp
    290                 295                 300

Pro Val Gly Gly Glu His Ala Asn Tyr Phe Ala Ala Gly Leu Lys Met
305                 310                 315                 320

Ala Asp Gln Val Val Val Val Ser Pro Gly Tyr Leu Trp Glu Leu Lys
                325                 330                 335

Thr Val Glu Gly Gly Trp Gly Leu His Asp Ile Ile Arg Gln Asn Asp
            340                 345                 350
```

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```
Trp Lys Thr Arg Gly Ile Val Asn Gly Ile Asp Asn Met Glu Trp Asn
    355             360             365
Pro Glu Val Asp Ala His Leu Lys Ser Asp Gly Tyr Thr Asn Phe Ser
    370             375             380
Leu Arg Thr Leu Asp Ser Gly Lys Arg Gln Cys Lys Glu Ala Leu Gln
385             390             395             400
Arg Glu Leu Gly Leu Gln Val Arg Ala Asp Val Pro Leu Leu Gly Phe
            405             410             415
Ile Gly Arg Leu Asp Gly Gln Lys Gly Val Glu Ile Ile Ala Asp Ala
            420             425             430
Met Pro Trp Ile Val Ser Gln Asp Val Gln Leu Val Met Leu Gly Thr
    435             440             445
Gly Arg His Asp Leu Glu Ser Met Leu Gln His Phe Glu Arg Glu His
    450             455             460
His Asp Lys Val Arg Gly Trp Val Gly Phe Ser Val Arg Leu Ala His
465             470             475             480
Arg Ile Thr Ala Gly Ala Asp Ala Leu Leu Met Pro Ser Arg Phe Val
            485             490             495
Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro
            500             505             510
Val Val His Ala Val Gly Gly Leu Arg Asp Thr Val Pro Pro Phe Asp
            515             520             525
Pro Phe Asn His Ser Gly Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala
    530             535             540
His Lys Leu Ile Glu Ala Leu Gly His Cys Leu Arg Thr Tyr Arg Asp
545             550             555             560
Phe Lys Glu Ser Trp Arg Ala Leu Gln Glu Arg Gly Met Ser Gln Asp
            565             570             575
Phe Ser Trp Glu His Ala Ala Lys Leu Tyr Glu Asp Val Leu Val Lys
            580             585             590
Ala Lys Tyr Gln Trp
            595
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<210> 7
<211> 5346
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (29)..(4912)

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cggcacgagg tttagtaggt tccgggaa atg gag atg tct ctc tgg cca cgg     52
                                Met Glu Met Ser Leu Trp Pro Arg
                                 1               5

agc ccc ctg tgc cct cgg agc agg cag ccg ctc gtc gtc gtc cgg ccg    100
Ser Pro Leu Cys Pro Arg Ser Arg Gln Pro Leu Val Val Val Arg Pro
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            10                    15                    20
gcc ggc cgc ggc ggc ctc acg cag cct ttt ttg atg aat ggc aga ttt      148
Ala Gly Arg Gly Gly Leu Thr Gln Pro Phe Leu Met Asn Gly Arg Phe
 25                  30                  35                  40

act cga agc agg acc ctt cga tgc atg gta gca agt tca gat cct cct      196
Thr Arg Ser Arg Thr Leu Arg Cys Met Val Ala Ser Ser Asp Pro Pro
                    45                  50                  55

aat agg aaa tca aga agg atg gta cca cct cag gtt aaa gtc att tct      244
Asn Arg Lys Ser Arg Arg Met Val Pro Pro Gln Val Lys Val Ile Ser
                60                  65                  70

tct aga gga tat acg aca aga ctc att gtt gaa cca agc aac gag aat      292
Ser Arg Gly Tyr Thr Thr Arg Leu Ile Val Glu Pro Ser Asn Glu Asn
            75                  80                  85

aca gaa cac aat aat cgg gat gaa gaa act ctt gat aca tac aat gcg      340
Thr Glu His Asn Asn Arg Asp Glu Glu Thr Leu Asp Thr Tyr Asn Ala
        90                  95                 100

cta tta agt acc gag aca gca gaa tgg aca gat aat aga gaa gcc gag      388
Leu Leu Ser Thr Glu Thr Ala Glu Trp Thr Asp Asn Arg Glu Ala Glu
105                 110                 115                 120

act gct aaa gcg gac tcg tcg caa aat gct tta agc agt tct ata att      436
Thr Ala Lys Ala Asp Ser Ser Gln Asn Ala Leu Ser Ser Ser Ile Ile
                125                 130                 135

ggg gaa gtg gat gtg gcg gat gaa gat ata ctt gcg gct gat ctg aca      484
Gly Glu Val Asp Val Ala Asp Glu Asp Ile Leu Ala Ala Asp Leu Thr
            140                 145                 150

gtg tat tca ttg agc agt gta atg aag aag gaa gtg gat gca gcg gac      532
Val Tyr Ser Leu Ser Ser Val Met Lys Lys Glu Val Asp Ala Ala Asp
            155                 160                 165

aaa gct aga gtt aaa gaa gac gca ttt gag ctg gat ttg cca gca act      580
Lys Ala Arg Val Lys Glu Asp Ala Phe Glu Leu Asp Leu Pro Ala Thr
        170                 175                 180

aca ttg aga agt gtg ata gta gat gtg atg gat cat aat ggg act gta      628
Thr Leu Arg Ser Val Ile Val Asp Val Met Asp His Asn Gly Thr Val
185                 190                 195                 200

caa gag aca ttg aga agt gtg ata gta gat gtg atg gat cat aat ggg      676
Gln Glu Thr Leu Arg Ser Val Ile Val Asp Val Met Asp His Asn Gly
                205                 210                 215

act gta caa gag aca ttg aga agt gtg ata gta gat gtg atg gat gat      724
Thr Val Gln Glu Thr Leu Arg Ser Val Ile Val Asp Val Met Asp Asp
                220                 225                 230

gcg gcg gac aaa gct aga gtt gaa gaa gac gta ttt gag ctg gat ttg      772
Ala Ala Asp Lys Ala Arg Val Glu Glu Asp Val Phe Glu Leu Asp Leu
            235                 240                 245

tca gga aat att tca agc agt gcg acg acc gtg gaa cta gat gcg gtt      820
Ser Gly Asn Ile Ser Ser Ser Ala Thr Thr Val Glu Leu Asp Ala Val
            250                 255                 260

gac gaa gtc ggg cct gtt caa gac aaa ttt gag gcg acc tca tca gga      868
Asp Glu Val Gly Pro Val Gln Asp Lys Phe Glu Ala Thr Ser Ser Gly
265                 270                 275                 280
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aat gtt tca aac agt gca acg gta cgg gaa gtg gat gca agt gat gaa    916
Asn Val Ser Asn Ser Ala Thr Val Arg Glu Val Asp Ala Ser Asp Glu
            285             290             295

gct ggg aat gat caa ggc ata ttt aga gca gat ttg tca gga aat gtt    964
Ala Gly Asn Asp Gln Gly Ile Phe Arg Ala Asp Leu Ser Gly Asn Val
            300             305             310

ttt tca agc agt aca aca gtg gaa gtg ggt gca gtg gat gaa gct ggg   1012
Phe Ser Ser Ser Thr Thr Val Glu Val Gly Ala Val Asp Glu Ala Gly
            315             320             325

tct ata aag gac agg ttt gag acg gat tcg tca gga aat gtt tca aca   1060
Ser Ile Lys Asp Arg Phe Glu Thr Asp Ser Ser Gly Asn Val Ser Thr
            330             335             340

agt gcg ccg atg tgg gat gca att gat gaa acc gtg gct gat caa gac   1108
Ser Ala Pro Met Trp Asp Ala Ile Asp Glu Thr Val Ala Asp Gln Asp
345             350             355             360

aca ttt gag gcg gat ttg tcg gga aat gct tca agc tgc gca aca tac   1156
Thr Phe Glu Ala Asp Leu Ser Gly Asn Ala Ser Ser Cys Ala Thr Tyr
            365             370             375

aga gaa gtg gat gat gtg gtg gat gaa act aga tca gaa gag gaa aca   1204
Arg Glu Val Asp Asp Val Val Asp Glu Thr Arg Ser Glu Glu Glu Thr
            380             385             390

ttt gca atg gat ttg ttt gca agt gaa tca ggc cat gag aaa cat atg   1252
Phe Ala Met Asp Leu Phe Ala Ser Glu Ser Gly His Glu Lys His Met
            395             400             405

gca gtg gat tat gtg ggt gaa gct acc gat gaa gaa gag act tac caa   1300
Ala Val Asp Tyr Val Gly Glu Ala Thr Asp Glu Glu Glu Thr Tyr Gln
            410             415             420

cag caa tat cca gta ccg tct tca ttc tct atg tgg gac aag gct att   1348
Gln Gln Tyr Pro Val Pro Ser Ser Phe Ser Met Trp Asp Lys Ala Ile
425             430             435             440

gct aaa aca ggt gta agt ttg aat cct gag ctg cga ctt gtc agg gtt   1396
Ala Lys Thr Gly Val Ser Leu Asn Pro Glu Leu Arg Leu Val Arg Val
            445             450             455

gaa gaa caa ggc aaa gta aat ttt agt gat aaa aaa gac ctg tca att   1444
Glu Glu Gln Gly Lys Val Asn Phe Ser Asp Lys Lys Asp Leu Ser Ile
            460             465             470

gat gat tta cca gga caa aac caa tcg atc att ggt tcc tat aaa caa   1492
Asp Asp Leu Pro Gly Gln Asn Gln Ser Ile Ile Gly Ser Tyr Lys Gln
            475             480             485

gat aaa tca att gct gat gtt gcg gga ccg acc caa tca att ttt ggt   1540
Asp Lys Ser Ile Ala Asp Val Ala Gly Pro Thr Gln Ser Ile Phe Gly
            490             495             500

tct agt aaa caa cac cgg tca att gtt gct ttc ccc aaa caa aac cag   1588
Ser Ser Lys Gln His Arg Ser Ile Val Ala Phe Pro Lys Gln Asn Gln
505             510             515             520

tca att gtt agt gtc act gag caa aag cag tcc ata gtt gga ttc cgt   1636
Ser Ile Val Ser Val Thr Glu Gln Lys Gln Ser Ile Val Gly Phe Arg
            525             530             535
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agt caa gat ctt tcg gct gtt agt ctc cct aaa caa aac gta cca att    1684
Ser Gln Asp Leu Ser Ala Val Ser Leu Pro Lys Gln Asn Val Pro Ile
            540                 545                 550

gtt ggt acg tcg aga gag ggt caa aca aag caa gtt cct gtt gtt gat    1732
Val Gly Thr Ser Arg Glu Gly Gln Thr Lys Gln Val Pro Val Val Asp
            555                 560                 565

aga cag gat gca ttg tat gtg aat gga ctg gaa gct aag gag gga gat    1780
Arg Gln Asp Ala Leu Tyr Val Asn Gly Leu Glu Ala Lys Glu Gly Asp
    570                 575                 580

cac aca tcc gag aaa act gat gag gat gcg ctt cat gta aag ttt aat    1828
His Thr Ser Glu Lys Thr Asp Glu Asp Ala Leu His Val Lys Phe Asn
585                 590                 595                 600

gtt gac aat gtg ttg cgg aag cat cag gca gat aga acc caa gca gtg    1876
Val Asp Asn Val Leu Arg Lys His Gln Ala Asp Arg Thr Gln Ala Val
            605                 610                 615

gaa aag aaa act tgg aag aaa gtt gat gag gaa cat ctt tac atg act    1924
Glu Lys Lys Thr Trp Lys Lys Val Asp Glu Glu His Leu Tyr Met Thr
            620                 625                 630

gaa cat cag aaa cgt gct gcc gaa gga cag atg gta gtt aac gag gat    1972
Glu His Gln Lys Arg Ala Ala Glu Gly Gln Met Val Val Asn Glu Asp
            635                 640                 645

gag ctt tct ata act gaa att gga atg ggg aga ggt gat aaa att cag    2020
Glu Leu Ser Ile Thr Glu Ile Gly Met Gly Arg Gly Asp Lys Ile Gln
    650                 655                 660

cat gtg ctt tct gag gaa gag ctt tca tgg tct gaa gat gaa gtg cag    2068
His Val Leu Ser Glu Glu Glu Leu Ser Trp Ser Glu Asp Glu Val Gln
665                 670                 675                 680

tta att gag gat gat gga caa tat gaa gtt gac gag acc tct gtg tcc    2116
Leu Ile Glu Asp Asp Gly Gln Tyr Glu Val Asp Glu Thr Ser Val Ser
                685                 690                 695

gtt aac gtt gaa caa gat atc cag ggg tca cca cag gat gtt gtg gat    2164
Val Asn Val Glu Gln Asp Ile Gln Gly Ser Pro Gln Asp Val Val Asp
            700                 705                 710

ccg caa gca cta aag gtg atg ctg caa gaa ctc gct gag aaa aat tat    2212
Pro Gln Ala Leu Lys Val Met Leu Gln Glu Leu Ala Glu Lys Asn Tyr
            715                 720                 725

tcg atg agg aac aag ctg ttt gtt ttt cca gag gta gtg aaa gct gat    2260
Ser Met Arg Asn Lys Leu Phe Val Phe Pro Glu Val Val Lys Ala Asp
    730                 735                 740

tca gtt att gat ctt tat tta aat cgt gac cta aca gct ttg gcg aat    2308
Ser Val Ile Asp Leu Tyr Leu Asn Arg Asp Leu Thr Ala Leu Ala Asn
745                 750                 755                 760

gaa ccc gat gtc gtc atc aaa gga gca ttc aat ggt tgg aaa tgg agg    2356
Glu Pro Asp Val Val Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg
            765                 770                 775

ctt ttc act gaa aga ttg cac aag agt gac ctt gga ggg gtt tgg tgg    2404
Leu Phe Thr Glu Arg Leu His Lys Ser Asp Leu Gly Gly Val Trp Trp
            780                 785                 790

tct tgc aaa ctg tac ata ccc aag gag gcc tac aga tta gac ttt gtg    2452
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Ser Cys Lys Leu Tyr Ile Pro Lys Glu Ala Tyr Arg Leu Asp Phe Val
        795             800             805

ttc ttc aac ggt cgc acg gtc tat gag aac aat ggc aac aat gat ttc    2500
Phe Phe Asn Gly Arg Thr Val Tyr Glu Asn Asn Gly Asn Asn Asp Phe
    810             815             820

tgt ata gga ata gaa ggc act atg aat gaa gat ctg ttt gag gat ttc    2548
Cys Ile Gly Ile Glu Gly Thr Met Asn Glu Asp Leu Phe Glu Asp Phe
825             830             835             840

ttg gtt aaa gaa aag caa agg gag ctt gag aaa ctt gcc atg gaa gaa    2596
Leu Val Lys Glu Lys Gln Arg Glu Leu Glu Lys Leu Ala Met Glu Glu
            845             850             855

gct gaa agg agg aca cag act gaa gaa cag cgg cga aga aag gaa gca    2644
Ala Glu Arg Arg Thr Gln Thr Glu Glu Gln Arg Arg Arg Lys Glu Ala
            860             865             870

agg gct gca gat gaa gct gtc agg gca caa gcg aag gcc gag ata gag    2692
Arg Ala Ala Asp Glu Ala Val Arg Ala Gln Ala Lys Ala Glu Ile Glu
        875             880             885

atc aag aag aaa aaa ttg caa agt atg ttg agt ttg gcc aga aca tgt    2740
Ile Lys Lys Lys Lys Leu Gln Ser Met Leu Ser Leu Ala Arg Thr Cys
        890             895             900

gtt gat aat ttg tgg tac ata gag gct agc aca gat aca aga gga gat    2788
Val Asp Asn Leu Trp Tyr Ile Glu Ala Ser Thr Asp Thr Arg Gly Asp
905             910             915             920

act atc agg tta tat tat aac aga aac tcg agg cca ctt gcg cat agt    2836
Thr Ile Arg Leu Tyr Tyr Asn Arg Asn Ser Arg Pro Leu Ala His Ser
            925             930             935

act gag att tgg atg cat ggt ggt tac aac aat tgg aca gat gga ctc    2884
Thr Glu Ile Trp Met His Gly Gly Tyr Asn Asn Trp Thr Asp Gly Leu
            940             945             950

tct att gtt gaa agc ttt gtc aag tgc aat gac aaa gac ggc gat tgg    2932
Ser Ile Val Glu Ser Phe Val Lys Cys Asn Asp Lys Asp Gly Asp Trp
        955             960             965

tgg tat gca gat gtt att cca cct gaa aag gca ctt gtg ttg gac tgg    2980
Trp Tyr Ala Asp Val Ile Pro Pro Glu Lys Ala Leu Val Leu Asp Trp
        970             975             980

gtt ttt gct gat ggg cca gct ggg aat gca agg aac tat gac aac aat    3028
Val Phe Ala Asp Gly Pro Ala Gly Asn Ala Arg Asn Tyr Asp Asn Asn
985             990             995             1000

gct cga caa gat ttc cat gct att ctt ccg aac aac aat gta acc gag    3076
Ala Arg Gln Asp Phe His Ala Ile Leu Pro Asn Asn Asn Val Thr Glu
            1005            1010            1015

gaa ggc ttc tgg gcg caa gag gag caa aac atc tat aca agg ctt ctg    3124
Glu Gly Phe Trp Ala Gln Glu Glu Gln Asn Ile Tyr Thr Arg Leu Leu
            1020            1025            1030

caa gaa agg aga gaa aag gaa gaa acc atg aaa aga aag gct gag aga    3172
Gln Glu Arg Arg Glu Lys Glu Glu Thr Met Lys Arg Lys Ala Glu Arg
        1035            1040            1045

agt gca aat atc aaa gct gag atg aag gca aaa act atg cga agg ttt    3220
Ser Ala Asn Ile Lys Ala Glu Met Lys Ala Lys Thr Met Arg Arg Phe
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     1050                1055                1060

ctg ctt tcc cag aaa cac att gtt tat acc gaa ccg ctt gaa ata cgt    3268
Leu Leu Ser Gln Lys His Ile Val Tyr Thr Glu Pro Leu Glu Ile Arg
1065                1070                1075                1080

gcc gga acc aca gtg gat gtg cta tac aat ccc tct aac aca gtg cta    3316
Ala Gly Thr Thr Val Asp Val Leu Tyr Asn Pro Ser Asn Thr Val Leu
                1085                1090                1095

aat gga aag tcg gag ggt tgg ttt aga tgc tcc ttt aac ctt tgg atg    3364
Asn Gly Lys Ser Glu Gly Trp Phe Arg Cys Ser Phe Asn Leu Trp Met
            1100                1105                1110

cat tca agt ggg gca ttg cca ccc cag aag atg gtg aaa tca ggg gat    3412
His Ser Ser Gly Ala Leu Pro Pro Gln Lys Met Val Lys Ser Gly Asp
        1115                1120                1125

ggg ccg ctc tta aaa gca aca gtt gat gtt cca ccg gat gcc tat atg    3460
Gly Pro Leu Leu Lys Ala Thr Val Asp Val Pro Pro Asp Ala Tyr Met
    1130                1135                1140

atg gac ttt gtt ttc tcc gag tgg gaa gaa gat ggg atc tat gac aac    3508
Met Asp Phe Val Phe Ser Glu Trp Glu Glu Asp Gly Ile Tyr Asp Asn
1145                1150                1155                1160

agg aat ggg atg gac tat cat att cct gtt tct gat tca att gaa aca    3556
Arg Asn Gly Met Asp Tyr His Ile Pro Val Ser Asp Ser Ile Glu Thr
            1165                1170                1175

gag aat tac atg cgt att atc cac att gcc gtt gag atg gcc ccc gtt    3604
Glu Asn Tyr Met Arg Ile Ile His Ile Ala Val Glu Met Ala Pro Val
        1180                1185                1190

gca aag gtt gga ggt ctt ggg gat gtt gtt aca agt ctt tca cgt gcc    3652
Ala Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala
    1195                1200                1205

att caa gat cta gga cat act gtc gag gtt att ctc ccg aag tac gac    3700
Ile Gln Asp Leu Gly His Thr Val Glu Val Ile Leu Pro Lys Tyr Asp
    1210                1215                1220

tgt ttg aac caa agc agt gtc aag gat tta cat tta tat caa agt ttt    3748
Cys Leu Asn Gln Ser Ser Val Lys Asp Leu His Leu Tyr Gln Ser Phe
1225                1230                1235                1240

tct tgg ggt ggt aca gaa ata aaa gta tgg gtt gga cga gtc gaa gac    3796
Ser Trp Gly Gly Thr Glu Ile Lys Val Trp Val Gly Arg Val Glu Asp
                1245                1250                1255

ctg acc gtt tac ttc ctg gaa cct caa aat ggg atg ttt ggc gtt gga    3844
Leu Thr Val Tyr Phe Leu Glu Pro Gln Asn Gly Met Phe Gly Val Gly
                1260                1265                1270

tgt gta tat gga agg aat gat gac cgc aga ttt ggg ttc ttc tgt cat    3892
Cys Val Tyr Gly Arg Asn Asp Asp Arg Arg Phe Gly Phe Phe Cys His
            1275                1280                1285

tct gct cta gag ttt atc ctc cag aat gaa ttt tct cca cat ata ata    3940
Ser Ala Leu Glu Phe Ile Leu Gln Asn Glu Phe Ser Pro His Ile Ile
        1290                1295                1300

cat tgc cat gat tgg tca agt gct ccg gtc gcc tgg cta tat aag gaa    3988
His Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Tyr Lys Glu
1305                1310                1315                1320
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cac tat tcc caa tcc aga atg gca agc act cgg gtt gta ttt acc atc     4036
His Tyr Ser Gln Ser Arg Met Ala Ser Thr Arg Val Val Phe Thr Ile
            1325             1330             1335

cac aat ctt gaa ttt gga gca cat tat att ggt aaa gca atg aca tac     4084
His Asn Leu Glu Phe Gly Ala His Tyr Ile Gly Lys Ala Met Thr Tyr
            1340             1345             1350

tgt gat aaa gcc aca act gtt tct cct aca tat tca agg gac gtg gca     4132
Cys Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Arg Asp Val Ala
        1355             1360             1365

ggc cat ggc gcc att gct cct cat cgt gag aaa ttc tac ggc att ctc     4180
Gly His Gly Ala Ile Ala Pro His Arg Glu Lys Phe Tyr Gly Ile Leu
      1370             1375             1380

aat gga att gat cca gat atc tgg gat ccg tac act gac aat ttt atc     4228
Asn Gly Ile Asp Pro Asp Ile Trp Asp Pro Tyr Thr Asp Asn Phe Ile
1385             1390             1395             1400

ccg gtc cct tat act tgt gag aat gtt gtc gaa ggc aag aga gct gca     4276
Pro Val Pro Tyr Thr Cys Glu Asn Val Val Glu Gly Lys Arg Ala Ala
            1405             1410             1415

aaa agg gcc ttg cag cag aag ttt gga tta cag caa act gat gtc cct     4324
Lys Arg Ala Leu Gln Gln Lys Phe Gly Leu Gln Gln Thr Asp Val Pro
            1420             1425             1430

att gtc gga atc atc acc cgt ctg aca gcc cag aag gga atc cac ctc     4372
Ile Val Gly Ile Ile Thr Arg Leu Thr Ala Gln Lys Gly Ile His Leu
            1435             1440             1445

atc aag cac gca att cac cga act ctc gaa agc aac gga cat gtg gtt     4420
Ile Lys His Ala Ile His Arg Thr Leu Glu Ser Asn Gly His Val Val
      1450             1455             1460

ttg ctt ggt tca gct cca gat cat cga ata caa ggc gat ttt tgc aga     4468
Leu Leu Gly Ser Ala Pro Asp His Arg Ile Gln Gly Asp Phe Cys Arg
1465             1470             1475             1480

ttg gcc gat gct ctt cat ggt gtt tac cat ggt agg gtg aag ctt gtt     4516
Leu Ala Asp Ala Leu His Gly Val Tyr His Gly Arg Val Lys Leu Val
            1485             1490             1495

cta acc tat gat gag cct ctt tct cac ctg ata tac gct ggc tcg gac     4564
Leu Thr Tyr Asp Glu Pro Leu Ser His Leu Ile Tyr Ala Gly Ser Asp
            1500             1505             1510

ttc ata att gtt cct tca atc ttc gaa ccc tgt ggc tta aca caa ctt     4612
Phe Ile Ile Val Pro Ser Ile Phe Glu Pro Cys Gly Leu Thr Gln Leu
            1515             1520             1525

gtt gcc atg cgt tat gga tcg atc cct ata gtt cgg aaa act gga gga     4660
Val Ala Met Arg Tyr Gly Ser Ile Pro Ile Val Arg Lys Thr Gly Gly
      1530             1535             1540

ctt cac gac aca gtc ttc gac gta gac aat gat aag gac cgg gct cgg     4708
Leu His Asp Thr Val Phe Asp Val Asp Asn Asp Lys Asp Arg Ala Arg
1545             1550             1555             1560

tct ctt ggt ctt gaa cca aat ggg ttc agt ttc gac gga gcc gac agc     4756
Ser Leu Gly Leu Glu Pro Asn Gly Phe Ser Phe Asp Gly Ala Asp Ser
            1565             1570             1575
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aat ggc gtg gat tat gcc ctc aac aga gca atc ggc gct tgg ttc gat   4804
Asn Gly Val Asp Tyr Ala Leu Asn Arg Ala Ile Gly Ala Trp Phe Asp
        1580                1585                1590

gcc cgt gat tgg ttc cac tcc ctg tgt aag agg gtc atg gag caa gac   4852
Ala Arg Asp Trp Phe His Ser Leu Cys Lys Arg Val Met Glu Gln Asp
        1595                1600                1605

tgg tcg tgg aac cgg ccc gca ctg gac tac att gaa ttg tac cat gcc   4900
Trp Ser Trp Asn Arg Pro Ala Leu Asp Tyr Ile Glu Leu Tyr His Ala
    1610                1615                1620

gct cga aaa ttc tgacacccaa ctgaaccaat gacaagaaca agcgcattgt       4952
Ala Arg Lys Phe
1625

gggatcgact agtcatacag ggctgtgcag atcgtcttgc ttcagttagt gccctcttca 5012

gttagttcca agcgcactac agtcgtacat agctgaggat cctcttgcct cctaccaggg 5072

ggaacaaagc agaaatgcat gagtgcattg ggaagacttt tatgtatatt gttaaaaaaa 5132

tttccttttc ttttccttcc ctgcacctgg aaatggttaa gcgcatcgcc gagataagaa 5192

ccgcagtgac attctgtgag tagctttgta tattctctca tcttgtgaaa actaatgttc 5252

atgttaggct gtctgatcat gtggaagctt tgttatatgt tacttatggt atacatcaat 5312

gatatttaca tttgtggaaa aaaaaaaaaa aaaa                              5346
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<210> 8
<211> 1628
<212> PRT
<213> Triticum aestivum

<400> 8
Met Glu Met Ser Leu Trp Pro Arg Ser Pro Leu Cys Pro Arg Ser Arg
 1               5                  10                  15

Gln Pro Leu Val Val Val Arg Pro Ala Gly Arg Gly Gly Leu Thr Gln
            20                  25                  30

Pro Phe Leu Met Asn Gly Arg Phe Thr Arg Ser Arg Thr Leu Arg Cys
        35                  40                  45

Met Val Ala Ser Ser Asp Pro Pro Asn Arg Lys Ser Arg Arg Met Val
    50                  55                  60

Pro Pro Gln Val Lys Val Ile Ser Ser Arg Gly Tyr Thr Thr Arg Leu
65                  70                  75                  80

Ile Val Glu Pro Ser Asn Glu Asn Thr Glu His Asn Asn Arg Asp Glu
                85                  90                  95

Glu Thr Leu Asp Thr Tyr Asn Ala Leu Leu Ser Thr Glu Thr Ala Glu
            100                 105                 110

Trp Thr Asp Asn Arg Glu Ala Glu Thr Ala Lys Ala Asp Ser Ser Gln
            115                 120                 125

Asn Ala Leu Ser Ser Ser Ile Ile Gly Glu Val Asp Val Ala Asp Glu
    130                 135                 140

Asp Ile Leu Ala Ala Asp Leu Thr Val Tyr Ser Leu Ser Ser Val Met
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145                     150                     155                     160

Lys Lys Glu Val Asp Ala Ala Asp Lys Ala Arg Val Lys Glu Asp Ala
            165                 170                 175

Phe Glu Leu Asp Leu Pro Ala Thr Thr Leu Arg Ser Val Ile Val Asp
            180                 185                 190

Val Met Asp His Asn Gly Thr Val Gln Glu Thr Leu Arg Ser Val Ile
        195                 200                 205

Val Asp Val Met Asp His Asn Gly Thr Val Gln Glu Thr Leu Arg Ser
    210                 215                 220

Val Ile Val Asp Val Met Asp Asp Ala Ala Asp Lys Ala Arg Val Glu
225                 230                 235                 240

Glu Asp Val Phe Glu Leu Asp Leu Ser Gly Asn Ile Ser Ser Ser Ala
            245                 250                 255

Thr Thr Val Glu Leu Asp Ala Val Asp Glu Val Gly Pro Val Gln Asp
            260                 265                 270

Lys Phe Glu Ala Thr Ser Ser Gly Asn Val Ser Asn Ser Ala Thr Val
        275                 280                 285

Arg Glu Val Asp Ala Ser Asp Glu Ala Gly Asn Asp Gln Gly Ile Phe
    290                 295                 300

Arg Ala Asp Leu Ser Gly Asn Val Phe Ser Ser Ser Thr Thr Val Glu
305                 310                 315                 320

Val Gly Ala Val Asp Glu Ala Gly Ser Ile Lys Asp Arg Phe Glu Thr
            325                 330                 335

Asp Ser Ser Gly Asn Val Ser Thr Ser Ala Pro Met Trp Asp Ala Ile
        340                 345                 350

Asp Glu Thr Val Ala Asp Gln Asp Thr Phe Glu Ala Asp Leu Ser Gly
        355                 360                 365

Asn Ala Ser Ser Cys Ala Thr Tyr Arg Glu Val Asp Asp Val Val Asp
    370                 375                 380

Glu Thr Arg Ser Glu Glu Glu Thr Phe Ala Met Asp Leu Phe Ala Ser
385                 390                 395                 400

Glu Ser Gly His Glu Lys His Met Ala Val Asp Tyr Val Gly Glu Ala
            405                 410                 415

Thr Asp Glu Glu Glu Thr Tyr Gln Gln Gln Tyr Pro Val Pro Ser Ser
        420                 425                 430

Phe Ser Met Trp Asp Lys Ala Ile Ala Lys Thr Gly Val Ser Leu Asn
        435                 440                 445

Pro Glu Leu Arg Leu Val Arg Val Glu Glu Gln Gly Lys Val Asn Phe
    450                 455                 460

Ser Asp Lys Lys Asp Leu Ser Ile Asp Asp Leu Pro Gly Gln Asn Gln
465                 470                 475                 480

Ser Ile Ile Gly Ser Tyr Lys Gln Asp Lys Ser Ile Ala Asp Val Ala
            485                 490                 495
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Gly Pro Thr Gln Ser Ile Phe Gly Ser Ser Lys Gln His Arg Ser Ile
        500             505             510

Val Ala Phe Pro Lys Gln Asn Gln Ser Ile Val Ser Val Thr Glu Gln
        515             520             525

Lys Gln Ser Ile Val Gly Phe Arg Ser Gln Asp Leu Ser Ala Val Ser
    530             535             540

Leu Pro Lys Gln Asn Val Pro Ile Val Gly Thr Ser Arg Glu Gly Gln
545             550             555             560

Thr Lys Gln Val Pro Val Val Asp Arg Gln Asp Ala Leu Tyr Val Asn
            565             570             575

Gly Leu Glu Ala Lys Glu Gly Asp His Thr Ser Glu Lys Thr Asp Glu
        580             585             590

Asp Ala Leu His Val Lys Phe Asn Val Asp Asn Val Leu Arg Lys His
        595             600             605

Gln Ala Asp Arg Thr Gln Ala Val Glu Lys Lys Thr Trp Lys Lys Val
    610             615             620

Asp Glu Glu His Leu Tyr Met Thr Glu His Gln Lys Arg Ala Ala Glu
625             630             635             640

Gly Gln Met Val Val Asn Glu Asp Glu Leu Ser Ile Thr Glu Ile Gly
            645             650             655

Met Gly Arg Gly Asp Lys Ile Gln His Val Leu Ser Glu Glu Glu Leu
        660             665             670

Ser Trp Ser Glu Asp Glu Val Gln Leu Ile Glu Asp Asp Gly Gln Tyr
        675             680             685

Glu Val Asp Glu Thr Ser Val Ser Val Asn Val Glu Gln Asp Ile Gln
        690             695             700

Gly Ser Pro Gln Asp Val Val Asp Pro Gln Ala Leu Lys Val Met Leu
705             710             715             720

Gln Glu Leu Ala Glu Lys Asn Tyr Ser Met Arg Asn Lys Leu Phe Val
            725             730             735

Phe Pro Glu Val Val Lys Ala Asp Ser Val Ile Asp Leu Tyr Leu Asn
            740             745             750

Arg Asp Leu Thr Ala Leu Ala Asn Glu Pro Asp Val Val Ile Lys Gly
        755             760             765

Ala Phe Asn Gly Trp Lys Trp Arg Leu Phe Thr Glu Arg Leu His Lys
    770             775             780

Ser Asp Leu Gly Gly Val Trp Trp Ser Cys Lys Leu Tyr Ile Pro Lys
785             790             795             800

Glu Ala Tyr Arg Leu Asp Phe Val Phe Phe Asn Gly Arg Thr Val Tyr
            805             810             815

Glu Asn Asn Gly Asn Asn Asp Phe Cys Ile Gly Ile Glu Gly Thr Met
            820             825             830

Asn Glu Asp Leu Phe Glu Asp Phe Leu Val Lys Glu Lys Gln Arg Glu
        835             840             845
```

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Leu Glu Lys Leu Ala Met Glu Glu Ala Glu Arg Arg Thr Gln Thr Glu
    850             855                 860

Glu Gln Arg Arg Arg Lys Glu Ala Arg Ala Ala Asp Glu Ala Val Arg
865             870                 875                 880

Ala Gln Ala Lys Ala Glu Ile Glu Ile Lys Lys Lys Lys Leu Gln Ser
                885                 890                 895

Met Leu Ser Leu Ala Arg Thr Cys Val Asp Asn Leu Trp Tyr Ile Glu
        900                 905                 910

Ala Ser Thr Asp Thr Arg Gly Asp Thr Ile Arg Leu Tyr Tyr Asn Arg
        915                 920                 925

Asn Ser Arg Pro Leu Ala His Ser Thr Glu Ile Trp Met His Gly Gly
    930                 935                 940

Tyr Asn Asn Trp Thr Asp Gly Leu Ser Ile Val Glu Ser Phe Val Lys
945                 950                 955                 960

Cys Asn Asp Lys Asp Gly Asp Trp Trp Tyr Ala Asp Val Ile Pro Pro
                965                 970                 975

Glu Lys Ala Leu Val Leu Asp Trp Val Phe Ala Asp Gly Pro Ala Gly
            980                 985                 990

Asn Ala Arg Asn Tyr Asp Asn Asn Ala Arg Gln Asp Phe His Ala Ile
            995                 1000                1005

Leu Pro Asn Asn Asn Val Thr Glu Glu Gly Phe Trp Ala Gln Glu Glu
    1010                1015                1020

Gln Asn Ile Tyr Thr Arg Leu Leu Gln Glu Arg Arg Glu Lys Glu Glu
025                 1030                1035                1040

Thr Met Lys Arg Lys Ala Glu Arg Ser Ala Asn Ile Lys Ala Glu Met
                1045                1050                1055

Lys Ala Lys Thr Met Arg Arg Phe Leu Leu Ser Gln Lys His Ile Val
            1060                1065                1070

Tyr Thr Glu Pro Leu Glu Ile Arg Ala Gly Thr Thr Val Asp Val Leu
        1075                1080                1085

Tyr Asn Pro Ser Asn Thr Val Leu Asn Gly Lys Ser Glu Gly Trp Phe
    1090                1095                1100

Arg Cys Ser Phe Asn Leu Trp Met His Ser Ser Gly Ala Leu Pro Pro
105                 1110                1115                1120

Gln Lys Met Val Lys Ser Gly Asp Gly Pro Leu Leu Lys Ala Thr Val
            1125                1130                1135

Asp Val Pro Pro Asp Ala Tyr Met Met Asp Phe Val Phe Ser Glu Trp
            1140                1145                1150

Glu Glu Asp Gly Ile Tyr Asp Asn Arg Asn Gly Met Asp Tyr His Ile
    1155                1160                1165

Pro Val Ser Asp Ser Ile Glu Thr Glu Asn Tyr Met Arg Ile Ile His
    1170                1175                1180

Ile Ala Val Glu Met Ala Pro Val Ala Lys Val Gly Gly Leu Gly Asp
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185              1190              1195              1200

Val Val Thr Ser Leu Ser Arg Ala Ile Gln Asp Leu Gly His Thr Val
            1205              1210              1215

Glu Val Ile Leu Pro Lys Tyr Asp Cys Leu Asn Gln Ser Ser Val Lys
         1220              1225              1230

Asp Leu His Leu Tyr Gln Ser Phe Ser Trp Gly Gly Thr Glu Ile Lys
      1235              1240              1245

Val Trp Val Gly Arg Val Glu Asp Leu Thr Val Tyr Phe Leu Glu Pro
   1250              1255              1260

Gln Asn Gly Met Phe Gly Val Gly Cys Val Tyr Gly Arg Asn Asp Asp
265              1270              1275              1280

Arg Arg Phe Gly Phe Phe Cys His Ser Ala Leu Glu Phe Ile Leu Gln
         1285              1290              1295

Asn Glu Phe Ser Pro His Ile Ile His Cys His Asp Trp Ser Ser Ala
      1300              1305              1310

Pro Val Ala Trp Leu Tyr Lys Glu His Tyr Ser Gln Ser Arg Met Ala
   1315              1320              1325

Ser Thr Arg Val Val Phe Thr Ile His Asn Leu Glu Phe Gly Ala His
   1330              1335              1340

Tyr Ile Gly Lys Ala Met Thr Tyr Cys Asp Lys Ala Thr Thr Val Ser
345              1350              1355              1360

Pro Thr Tyr Ser Arg Asp Val Ala Gly His Gly Ala Ile Ala Pro His
         1365              1370              1375

Arg Glu Lys Phe Tyr Gly Ile Leu Asn Gly Ile Asp Pro Asp Ile Trp
      1380              1385              1390

Asp Pro Tyr Thr Asp Asn Phe Ile Pro Val Pro Tyr Thr Cys Glu Asn
      1395              1400              1405

Val Val Glu Gly Lys Arg Ala Ala Lys Arg Ala Leu Gln Gln Lys Phe
   1410              1415              1420

Gly Leu Gln Gln Thr Asp Val Pro Ile Val Gly Ile Ile Thr Arg Leu
425              1430              1435              1440

Thr Ala Gln Lys Gly Ile His Leu Ile Lys His Ala Ile His Arg Thr
            1445              1450              1455

Leu Glu Ser Asn Gly His Val Val Leu Leu Gly Ser Ala Pro Asp His
         1460              1465              1470

Arg Ile Gln Gly Asp Phe Cys Arg Leu Ala Asp Ala Leu His Gly Val
   1475              1480              1485

Tyr His Gly Arg Val Lys Leu Val Leu Thr Tyr Asp Glu Pro Leu Ser
   1490              1495              1500

His Leu Ile Tyr Ala Gly Ser Asp Phe Ile Ile Val Pro Ser Ile Phe
505              1510              1515              1520

Glu Pro Cys Gly Leu Thr Gln Leu Val Ala Met Arg Tyr Gly Ser Ile
         1525              1530              1535
```

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```
Pro Ile Val Arg Lys Thr Gly Gly Leu His Asp Thr Val Phe Asp Val
        1540              1545              1550

Asp Asn Asp Lys Asp Arg Ala Arg Ser Leu Gly Leu Glu Pro Asn Gly
        1555              1560              1565

Phe Ser Phe Asp Gly Ala Asp Ser Asn Gly Val Asp Tyr Ala Leu Asn
    1570              1575              1580

Arg Ala Ile Gly Ala Trp Phe Asp Ala Arg Asp Trp Phe His Ser Leu
585              1590              1595              1600

Cys Lys Arg Val Met Glu Gln Asp Trp Ser Trp Asn Arg Pro Ala Leu
        1605              1610              1615

Asp Tyr Ile Glu Leu Tyr His Ala Ala Arg Lys Phe
        1620              1625
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<211> 3621
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(3177)

<400> 9
gat gca ttg tat gtg aat gga ctg gaa gct aag gag gga gat cac aca      48
Asp Ala Leu Tyr Val Asn Gly Leu Glu Ala Lys Glu Gly Asp His Thr
 1               5                  10                  15

tcc gag aaa act gat gag gat gcg ctt cat gta aag ttt aat gtt gac      96
Ser Glu Lys Thr Asp Glu Asp Ala Leu His Val Lys Phe Asn Val Asp
            20                  25                  30

aat gtg ttg cgg aag cat cag gca gat aga acc caa gca gtg gaa aag     144
Asn Val Leu Arg Lys His Gln Ala Asp Arg Thr Gln Ala Val Glu Lys
        35                  40                  45

aaa act tgg aag aaa gtt gat gag gaa cat ctt tac atg act gaa cat     192
Lys Thr Trp Lys Lys Val Asp Glu Glu His Leu Tyr Met Thr Glu His
    50                  55                  60

cag aaa cgt gct gcc gaa gga cag atg gta gtt aac gag gat gag ctt     240
Gln Lys Arg Ala Ala Glu Gly Gln Met Val Val Asn Glu Asp Glu Leu
65                  70                  75                  80

tct ata act gaa att gga atg ggg aga ggt gat aaa att cag cat gtg     288
Ser Ile Thr Glu Ile Gly Met Gly Arg Gly Asp Lys Ile Gln His Val
                85                  90                  95

ctt tct gag gaa gag ctt tca tgg tct gaa gat gaa gtg cag tta att     336
Leu Ser Glu Glu Glu Leu Ser Trp Ser Glu Asp Glu Val Gln Leu Ile
            100                 105                 110

gag gat gat gga caa tat gaa gtt gac gag acc tct gtg tcc gtt aac     384
Glu Asp Asp Gly Gln Tyr Glu Val Asp Glu Thr Ser Val Ser Val Asn
            115                 120                 125

gtt gaa caa gat atc cag ggg tca cca cag gat gtt gtg gat ccg caa     432
Val Glu Gln Asp Ile Gln Gly Ser Pro Gln Asp Val Val Asp Pro Gln
        130                 135                 140
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gca cta aag gtg atg ctg caa gaa ctc gct gag aaa aat tat tcg atg    480
Ala Leu Lys Val Met Leu Gln Glu Leu Ala Glu Lys Asn Tyr Ser Met
145             150                 155                 160

agg aac aag ctg ttt gtt ttt cca gag gta gtg aaa gct gat tca gtt    528
Arg Asn Lys Leu Phe Val Phe Pro Glu Val Val Lys Ala Asp Ser Val
                165                 170                 175

att gat ctt tat tta aat cgt gac cta aca gct ttg gcg aat gaa ccc    576
Ile Asp Leu Tyr Leu Asn Arg Asp Leu Thr Ala Leu Ala Asn Glu Pro
                180                 185                 190

gat gtc gtc atc aaa gga gca ttc aat ggt tgg aaa tgg agg ctt ttc    624
Asp Val Val Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg Leu Phe
                195                 200                 205

act gaa aga ttg cac aag agt gac ctt gga ggg gtt tgg tgg tct tgc    672
Thr Glu Arg Leu His Lys Ser Asp Leu Gly Gly Val Trp Trp Ser Cys
    210                 215                 220

aaa ctg tac ata ccc aag gag gcc tac aga tta gac ttt gtg ttc ttc    720
Lys Leu Tyr Ile Pro Lys Glu Ala Tyr Arg Leu Asp Phe Val Phe Phe
225                 230                 235                 240

aac ggt cgc acg gtc tat gag aac aat ggc aac aat gat ttc tgt ata    768
Asn Gly Arg Thr Val Tyr Glu Asn Asn Gly Asn Asn Asp Phe Cys Ile
                245                 250                 255

gga ata gaa ggc act atg aat gaa gat ctg ttt gag gat ttc ttg gtt    816
Gly Ile Glu Gly Thr Met Asn Glu Asp Leu Phe Glu Asp Phe Leu Val
                260                 265                 270

aaa gaa aag caa agg gag ctt gag aaa ctt gcc atg gaa gaa gct gaa    864
Lys Glu Lys Gln Arg Glu Leu Glu Lys Leu Ala Met Glu Glu Ala Glu
                275                 280                 285

agg agg aca cag act gaa gaa cag cgg cga aga aag gaa gca agg gct    912
Arg Arg Thr Gln Thr Glu Glu Gln Arg Arg Arg Lys Glu Ala Arg Ala
    290                 295                 300

gca gat gaa gct gtc agg gca caa gcg aag gcc gag ata gag atc aag    960
Ala Asp Glu Ala Val Arg Ala Gln Ala Lys Ala Glu Ile Glu Ile Lys
305                 310                 315                 320

aag aaa aaa ttg caa agt atg ttg agt ttg gcc aga aca tgt gtt gat   1008
Lys Lys Lys Leu Gln Ser Met Leu Ser Leu Ala Arg Thr Cys Val Asp
                325                 330                 335

aat ttg tgg tac ata gag gct agc aca gat aca aga gga gat act atc   1056
Asn Leu Trp Tyr Ile Glu Ala Ser Thr Asp Thr Arg Gly Asp Thr Ile
                340                 345                 350

agg tta tat tat aac aga aac tcg agg cca ctt gcg cat agt act gag   1104
Arg Leu Tyr Tyr Asn Arg Asn Ser Arg Pro Leu Ala His Ser Thr Glu
                355                 360                 365

att tgg atg cat ggt ggt tac aac aat tgg tca gat gga ctc tct att   1152
Ile Trp Met His Gly Gly Tyr Asn Asn Trp Ser Asp Gly Leu Ser Ile
    370                 375                 380

gtt gaa agc ttt gtc aag tgc aat gac aaa gac ggc gat tgg tgg tat   1200
Val Glu Ser Phe Val Lys Cys Asn Asp Lys Asp Gly Asp Trp Trp Tyr
385                 390                 395                 400

gca gat gtt att cca cct gaa aag gca ctt gtg ttg gac tgg gtt ttt   1248
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Ala Asp Val Ile Pro Pro Glu Lys Ala Leu Val Leu Asp Trp Val Phe
            405             410             415

gct gat ggg cca gct ggg aat gca agg aac tat gac aac aat gct cga   1296
Ala Asp Gly Pro Ala Gly Asn Ala Arg Asn Tyr Asp Asn Asn Ala Arg
        420             425             430

caa gat ttc cat gct att ctt ccg aac aac aat gta acc gag gaa ggc   1344
Gln Asp Phe His Ala Ile Leu Pro Asn Asn Asn Val Thr Glu Glu Gly
        435             440             445

ttc tgg gcg caa gag gag caa aac atc tat aca agg ctt ctg caa gaa   1392
Phe Trp Ala Gln Glu Glu Gln Asn Ile Tyr Thr Arg Leu Leu Gln Glu
        450             455             460

agg aga gaa aag gaa gaa acc atg aaa aga aag gct gag aga agt gca   1440
Arg Arg Glu Lys Glu Glu Thr Met Lys Arg Lys Ala Glu Arg Ser Ala
465             470             475             480

aat atc aaa gct gag atg aag gca aaa act atg cga agg ttt ctg ctt   1488
Asn Ile Lys Ala Glu Met Lys Ala Lys Thr Met Arg Arg Phe Leu Leu
            485             490             495

tcc cag aaa cac att gtt tat acc cga acc gnc ttg aaa tac gtg ccc   1536
Ser Gln Lys His Ile Val Tyr Thr Arg Thr Xaa Leu Lys Tyr Val Pro
            500             505             510

gga acc aca gtg gat gtg cta tac aat ccc tct aac aca gtg cta aat   1584
Gly Thr Thr Val Asp Val Leu Tyr Asn Pro Ser Asn Thr Val Leu Asn
            515             520             525

gga aag tcg gag ggt tgg ttt aga tgc tcc ttt aac ctt tgg atg cat   1632
Gly Lys Ser Glu Gly Trp Phe Arg Cys Ser Phe Asn Leu Trp Met His
        530             535             540

tca agt ggg gca ttg cca ccc cag aag atg gtg aaa tca ggg gat ggg   1680
Ser Ser Gly Ala Leu Pro Pro Gln Lys Met Val Lys Ser Gly Asp Gly
545             550             555             560

ccg ctc tta aaa gca aca gtt gat gtt cca ccg gat gcc tat atg atg   1728
Pro Leu Leu Lys Ala Thr Val Asp Val Pro Pro Asp Ala Tyr Met Met
            565             570             575

gac ttt gtt ttc tcc gag tgg gaa gaa gat ggg atc tat gac aac agg   1776
Asp Phe Val Phe Ser Glu Trp Glu Glu Asp Gly Ile Tyr Asp Asn Arg
        580             585             590

aat ggg atg gac tat cat att cct gtt tct gat tca att gaa aca gag   1824
Asn Gly Met Asp Tyr His Ile Pro Val Ser Asp Ser Ile Glu Thr Glu
        595             600             605

aat tac atg cgt att atc cac att gcc gtt gag atg gcc ccc gtt gca   1872
Asn Tyr Met Arg Ile Ile His Ile Ala Val Glu Met Ala Pro Val Ala
        610             615             620

aag gtt gga ggt ctt ggg gat gtt gtt aca agt ctt tca cgt gcc att   1920
Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Ile
625             630             635             640

caa gat cta gga cat act gtc gag gtt att ctc ccg aag tac gac tgt   1968
Gln Asp Leu Gly His Thr Val Glu Val Ile Leu Pro Lys Tyr Asp Cys
            645             650             655

ttg aac caa agc agt gtc aag gat tta cat tta tat caa agt ttt tct   2016
Leu Asn Gln Ser Ser Val Lys Asp Leu His Leu Tyr Gln Ser Phe Ser
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                    660              665              670

tgg ggt ggt aca gaa ata aaa gta tgg gtt gga cga gtc gaa gac ctg    2064
Trp Gly Gly Thr Glu Ile Lys Val Trp Val Gly Arg Val Glu Asp Leu
        675              680              685

acc gtt tac ttc ctg gaa cct caa aat ggg atg ttt ggc gtt gga tgt    2112
Thr Val Tyr Phe Leu Glu Pro Gln Asn Gly Met Phe Gly Val Gly Cys
    690              695              700

gta tat gga agg aat gat gac cgc aga ttt ggg ttc ttc tgt cat tct    2160
Val Tyr Gly Arg Asn Asp Asp Arg Arg Phe Gly Phe Phe Cys His Ser
705              710              715              720

gct cta gag ttt atc ctc cag aat gaa ttt tct cca cat ata ata cat    2208
Ala Leu Glu Phe Ile Leu Gln Asn Glu Phe Ser Pro His Ile Ile His
                725              730              735

tgc cat gat tgg tca agt gct ccg gtc gcc tgg cta tat aag gaa cac    2256
Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Tyr Lys Glu His
            740              745              750

tat tcc caa tcc aga atg gca agc act cgg gtt gta ttt acc atc cac    2304
Tyr Ser Gln Ser Arg Met Ala Ser Thr Arg Val Val Phe Thr Ile His
        755              760              765

aat ctt gaa ttt gga gca cat tat att ggt aaa gca atg aca tac tgt    2352
Asn Leu Glu Phe Gly Ala His Tyr Ile Gly Lys Ala Met Thr Tyr Cys
    770              775              780

gat aaa gcc aca act gtt tct cct aca tat tca agg gac gtg gca ggc    2400
Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Arg Asp Val Ala Gly
785              790              795              800

cat ggc gcc att gct cct cat cgt gag aaa ttc tac ggc att ctc aat    2448
His Gly Ala Ile Ala Pro His Arg Glu Lys Phe Tyr Gly Ile Leu Asn
                805              810              815

gga att gat cca gat atc tgg gat ccg tac act gac aat ttt atc ccg    2496
Gly Ile Asp Pro Asp Ile Trp Asp Pro Tyr Thr Asp Asn Phe Ile Pro
            820              825              830

gtc cct tat act tgt gag aat gtt gtc gaa ggc aag agg gct gca aaa    2544
Val Pro Tyr Thr Cys Glu Asn Val Val Glu Gly Lys Arg Ala Ala Lys
        835              840              845

agg gcc ttg cag cag aag ttt gga tta cag caa act gat gtc cct att    2592
Arg Ala Leu Gln Gln Lys Phe Gly Leu Gln Gln Thr Asp Val Pro Ile
        850              855              860

gtc gga atc atc acc cgt ctg aca gca cag aag gga atc cac ctc atc    2640
Val Gly Ile Ile Thr Arg Leu Thr Ala Gln Lys Gly Ile His Leu Ile
865              870              875              880

aag cac gca att cac cga acc ctc gag agc aat gga caa gtg gtt ttg    2688
Lys His Ala Ile His Arg Thr Leu Glu Ser Asn Gly Gln Val Val Leu
                885              890              895

ctt ggt tca gct cca gat cat cga ata caa ggc gat ttt tgc aga ttg    2736
Leu Gly Ser Ala Pro Asp His Arg Ile Gln Gly Asp Phe Cys Arg Leu
            900              905              910

gcc gat gct ctt cac ggt gtt tac cat ggt agg gtg aag ctt gtt cta    2784
Ala Asp Ala Leu His Gly Val Tyr His Gly Arg Val Lys Leu Val Leu
        915              920              925
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```
acc tac gat gag cct ctt tct cac ctg ata tac gct ggc tcc gac ttc    2832
Thr Tyr Asp Glu Pro Leu Ser His Leu Ile Tyr Ala Gly Ser Asp Phe
    930             935             940

att att gtc cct tca atc ttt gaa ccc tgt ggc tta aca caa ctt gtt    2880
Ile Ile Val Pro Ser Ile Phe Glu Pro Cys Gly Leu Thr Gln Leu Val
945             950             955             960

gcc atg cgt tat gga tcg atc cct ata gtt cgg aaa acc gga gga ctt    2928
Ala Met Arg Tyr Gly Ser Ile Pro Ile Val Arg Lys Thr Gly Gly Leu
            965             970             975

tac gac act gtc ttc gac gta gac aat gat aag gac cgg gct cgg tct    2976
Tyr Asp Thr Val Phe Asp Val Asp Asn Asp Lys Asp Arg Ala Arg Ser
        980             985             990

ctt ggt ctt gaa cca aat ggg ttc agt ttc gac gga gcc gac agc aat    3024
Leu Gly Leu Glu Pro Asn Gly Phe Ser Phe Asp Gly Ala Asp Ser Asn
        995             1000            1005

ggc gtg gat tat gcc ctc aac aga gca atc ggc gct tgg ttc gat gcc    3072
Gly Val Asp Tyr Ala Leu Asn Arg Ala Ile Gly Ala Trp Phe Asp Ala
    1010            1015            1020

cgt gat tgg ttc cac tcc ctg tgt aag agg gtc atg gag caa gac tgg    3120
Arg Asp Trp Phe His Ser Leu Cys Lys Arg Val Met Glu Gln Asp Trp
1025            1030            1035            1040

tcg tgg aac cgg cct gca ctg gac tac att gaa ttg tac cat gcc gct    3168
Ser Trp Asn Arg Pro Ala Leu Asp Tyr Ile Glu Leu Tyr His Ala Ala
            1045            1050            1055

cga aaa ttc tgacacccaa ctgaaccaat ggcaagaaca agcgcattgt            3217
Arg Lys Phe

gggatcgact acagtcatac agggctgtgc agatcgtctt gcttcagtta gtgccctctt 3277

cagttagttc caagcgcact acagtcgtac atagctgagg atcctcttgc ctcctccacc 3337

aggggaaaca aagcagaaat gcataagtgc attgggaaga cttttatgta tattgttaaa 3397

ttttccttt tctttttcctt ccctgcacct ggaaatggtt aagcgcatcg ccgagataag 3457

aaccacagta acattctgtg agtagctttg tatattctct catcttgtga aaactaatgt 3517

gcatgttagg ctctctgatc atgtggaagc tttgttatat gttacttatg gttatatggt 3577

atacatcaat gatatttaca tttgtggaaa aaaaaaa~aa aaaa                  3621
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<210> 10
<211> 1059
<212> PRT
<213> Triticum aestivum

<400> 10
Asp Ala Leu Tyr Val Asn Gly Leu Glu Ala Lys Glu Gly Asp His Thr
  1             5              10              15

Ser Glu Lys Thr Asp Glu Asp Ala Leu His Val Lys Phe Asn Val Asp
            20              25              30

Asn Val Leu Arg Lys His Gln Ala Asp Arg Thr Gln Ala Val Glu Lys
      35              40              45
```

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```
Lys Thr Trp Lys Lys Val Asp Glu Glu His Leu Tyr Met Thr Glu His
    50              55              60
Gln Lys Arg Ala Ala Glu Gly Gln Met Val Val Asn Glu Asp Glu Leu
65              70              75              80
Ser Ile Thr Glu Ile Gly Met Gly Arg Gly Asp Lys Ile Gln His Val
            85              90              95
Leu Ser Glu Glu Glu Leu Ser Trp Ser Glu Asp Glu Val Gln Leu Ile
        100             105             110
Glu Asp Asp Gly Gln Tyr Glu Val Asp Glu Thr Ser Val Ser Val Asn
        115             120             125
Val Glu Gln Asp Ile Gln Gly Ser Pro Gln Asp Val Val Asp Pro Gln
    130             135             140
Ala Leu Lys Val Met Leu Gln Glu Leu Ala Glu Lys Asn Tyr Ser Met
145             150             155             160
Arg Asn Lys Leu Phe Val Phe Pro Glu Val Val Lys Ala Asp Ser Val
            165             170             175
Ile Asp Leu Tyr Leu Asn Arg Asp Leu Thr Ala Leu Ala Asn Glu Pro
            180             185             190
Asp Val Val Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg Leu Phe
        195             200             205
Thr Glu Arg Leu His Lys Ser Asp Leu Gly Gly Val Trp Trp Ser Cys
    210             215             220
Lys Leu Tyr Ile Pro Lys Glu Ala Tyr Arg Leu Asp Phe Val Phe Phe
225             230             235             240
Asn Gly Arg Thr Val Tyr Glu Asn Asn Gly Asn Asn Asp Phe Cys Ile
            245             250             255
Gly Ile Glu Gly Thr Met Asn Glu Asp Leu Phe Glu Asp Phe Leu Val
        260             265             270
Lys Glu Lys Gln Arg Glu Leu Glu Lys Leu Ala Met Glu Glu Ala Glu
        275             280             285
Arg Arg Thr Gln Thr Glu Glu Gln Arg Arg Arg Lys Glu Ala Arg Ala
    290             295             300
Ala Asp Glu Ala Val Arg Ala Gln Ala Lys Ala Glu Ile Glu Ile Lys
305             310             315             320
Lys Lys Lys Leu Gln Ser Met Leu Ser Leu Ala Arg Thr Cys Val Asp
            325             330             335
Asn Leu Trp Tyr Ile Glu Ala Ser Thr Asp Thr Arg Gly Asp Thr Ile
            340             345             350
Arg Leu Tyr Tyr Asn Arg Asn Ser Arg Pro Leu Ala His Ser Thr Glu
        355             360             365
Ile Trp Met His Gly Gly Tyr Asn Asn Trp Ser Asp Gly Leu Ser Ile
    370             375             380
Val Glu Ser Phe Val Lys Cys Asn Asp Lys Asp Gly Asp Trp Trp Tyr
```

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385                    390                    395                    400

Ala Asp Val Ile Pro Pro Glu Lys Ala Leu Val Leu Asp Trp Val Phe
            405                 410                 415

Ala Asp Gly Pro Ala Gly Asn Ala Arg Asn Tyr Asp Asn Asn Ala Arg
            420                 425                 430

Gln Asp Phe His Ala Ile Leu Pro Asn Asn Asn Val Thr Glu Glu Gly
            435                 440                 445

Phe Trp Ala Gln Glu Glu Gln Asn Ile Tyr Thr Arg Leu Leu Gln Glu
    450                 455                 460

Arg Arg Glu Lys Glu Glu Thr Met Lys Arg Lys Ala Glu Arg Ser Ala
465                 470                 475                 480

Asn Ile Lys Ala Glu Met Lys Ala Lys Thr Met Arg Arg Phe Leu Leu
            485                 490                 495

Ser Gln Lys His Ile Val Tyr Thr Arg Thr Xaa Leu Lys Tyr Val Pro
            500                 505                 510

Gly Thr Thr Val Asp Val Leu Tyr Asn Pro Ser Asn Thr Val Leu Asn
            515                 520                 525

Gly Lys Ser Glu Gly Trp Phe Arg Cys Ser Phe Asn Leu Trp Met His
            530                 535                 540

Ser Ser Gly Ala Leu Pro Pro Gln Lys Met Val Lys Ser Gly Asp Gly
545                 550                 555                 560

Pro Leu Leu Lys Ala Thr Val Asp Val Pro Pro Asp Ala Tyr Met Met
            565                 570                 575

Asp Phe Val Phe Ser Glu Trp Glu Glu Asp Gly Ile Tyr Asp Asn Arg
            580                 585                 590

Asn Gly Met Asp Tyr His Ile Pro Val Ser Asp Ser Ile Glu Thr Glu
            595                 600                 605

Asn Tyr Met Arg Ile Ile His Ile Ala Val Glu Met Ala Pro Val Ala
    610                 615                 620

Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Ile
625                 630                 635                 640

Gln Asp Leu Gly His Thr Val Glu Val Ile Leu Pro Lys Tyr Asp Cys
            645                 650                 655

Leu Asn Gln Ser Ser Val Lys Asp Leu His Leu Tyr Gln Ser Phe Ser
            660                 665                 670

Trp Gly Gly Thr Glu Ile Lys Val Trp Val Gly Arg Val Glu Asp Leu
    675                 680                 685

Thr Val Tyr Phe Leu Glu Pro Gln Asn Gly Met Phe Gly Val Gly Cys
    690                 695                 700

Val Tyr Gly Arg Asn Asp Asp Arg Arg Phe Gly Phe Phe Cys His Ser
705                 710                 715                 720

Ala Leu Glu Phe Ile Leu Gln Asn Glu Phe Ser Pro His Ile Ile His
            725                 730                 735
```

```
Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Tyr Lys Glu His
            740             745             750

Tyr Ser Gln Ser Arg Met Ala Ser Thr Arg Val Val Phe Thr Ile His
        755             760             765

Asn Leu Glu Phe Gly Ala His Tyr Ile Gly Lys Ala Met Thr Tyr Cys
    770             775             780

Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Arg Asp Val Ala Gly
785             790             795             800

His Gly Ala Ile Ala Pro His Arg Glu Lys Phe Tyr Gly Ile Leu Asn
            805             810             815

Gly Ile Asp Pro Asp Ile Trp Asp Pro Tyr Thr Asp Asn Phe Ile Pro
            820             825             830

Val Pro Tyr Thr Cys Glu Asn Val Val Glu Gly Lys Arg Ala Ala Lys
        835             840             845

Arg Ala Leu Gln Gln Lys Phe Gly Leu Gln Gln Thr Asp Val Pro Ile
    850             855             860

Val Gly Ile Ile Thr Arg Leu Thr Ala Gln Lys Gly Ile His Leu Ile
865             870             875             880

Lys His Ala Ile His Arg Thr Leu Glu Ser Asn Gly Gln Val Val Leu
            885             890             895

Leu Gly Ser Ala Pro Asp His Arg Ile Gln Gly Asp Phe Cys Arg Leu
        900             905             910

Ala Asp Ala Leu His Gly Val Tyr His Gly Arg Val Lys Leu Val Leu
    915             920             925

Thr Tyr Asp Glu Pro Leu Ser His Leu Ile Tyr Ala Gly Ser Asp Phe
    930             935             940

Ile Ile Val Pro Ser Ile Phe Glu Pro Cys Gly Leu Thr Gln Leu Val
945             950             955             960

Ala Met Arg Tyr Gly Ser Ile Pro Ile Val Arg Lys Thr Gly Gly Leu
            965             970             975

Tyr Asp Thr Val Phe Asp Val Asp Asn Asp Lys Asp Arg Ala Arg Ser
        980             985             990

Leu Gly Leu Glu Pro Asn Gly Phe Ser Phe Asp Gly Ala Asp Ser Asn
    995             1000            1005

Gly Val Asp Tyr Ala Leu Asn Arg Ala Ile Gly Ala Trp Phe Asp Ala
    1010            1015            1020

Arg Asp Trp Phe His Ser Leu Cys Lys Arg Val Met Glu Gln Asp Trp
1025            1030            1035            1040

Ser Trp Asn Arg Pro Ala Leu Asp Tyr Ile Glu Leu Tyr His Ala Ala
            1045            1050            1055

Arg Lys Phe
```

<210> 11
<211> 728

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```
<212> DNA
<213> Triticum sp.

<400> 11
gatcttgaac ggcacgtgaa agacttgtaa caacatcccc gagacctcca acctatgaga 60

tcatcgatca tgacagagca tagtattatg gcatagaatg aaaaaaaggc ataaggtgat 120

gagatctcca cgccagagcg ttgtattcca attttagttc tttccccgtg aggaggggag 180

gctaggcggg cgaggcagag gggatagggc agtcgccgct gcgtggtgga ctgactggtg 240

tggtgggtgg tgggttttgc gggcggggtt tagtaggttc ccggaaatgg agatggctct 300

ccggccacgg agccctctgt gccctcggag cagtcagccg ctcgtcgtcg tccggccggc 360

cggccgcggc ggcggcctcg cgcaggtacg ggtgattatg gttcttgatt cggtcggttc 420

acggaatgtt gtttgatttg gttctgtccc gggtcaggtt catagtgatt ttattccgca 480

aaaaaaaaag gtttatagtg attttgattt ctttcatctc gggaacattt ttatatctgg 540

gagtcaaagg gcattggttt tgatttgcat gcggaacata ttggttattt attaatgtgg 600

tgagctggaa ttcatactgc ttaaaacgac gtgattttaa ttgctggaag aggtaaagaa 660

catgaattct tgttatattt gttaaaaaaa atcccctgtt ctagcgtttc aatctgcatg 720

atcatgga                                                            728


<210> 12
<211> 2446
<212> DNA
<213> Triticum sp.

<400> 12
gtgggtctat aaaagacagg tttgagcgga ttcgtcagga aatgtttcaa caagtgcgac 60

gatgtgggat gcaattgatg aaaccgtggc ttgatcaaga cgcagttgag gcggatttgt 120

cgggaaatgc ttcaagctgc gcgacataca gagaagtgga tgatgtggtg gatgaaacta 180

gatcagaaga ggaaacattt gcgatggatt tgtttgcaag tgaatcaggc catgagaaac 240

atatggcagt ggatcatgtg ggtgaagcta ccgatgaaga agagacttac caacagcaat 300

atccagtacc gtcttcattc tctatgtggg acaaggctat tgctaaaaca ggtgtaagtt 36^

tgaatcctga gctgcgactt gtcagggttg aagaacaagg caaagtaaat tttagtgata 420

aaaaagacct gtcaattgat gatttaccag gacaaaacca atcgatcatt ggttcctata 480

aacaagataa atcaattgct gatgttgcgg gaccgaccca atcaattttt ggttctagta 540

aacaacaccg gtcaattgtt gctttcccca aacaaaacca gtcaattgtt agtgtcactg 600

agcaaaagca gtccatagtt ggattccgta gtcaagatct ttcggctgtt agtctcccta 660

aacaaaacgt accaattgtt ggtacgtcga gagagggtca aacaaagcaa gttcctgttg 720

ttgatagaca ggatgcgttg tatgtgaatg gactggaagc taaggaggga gatcacacat 780

ccgagaaaac cgatgaggat gtgcttcatg taaaatttaa tgttgacaat gtgttgcgga 840
```

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```
agcatcaggc agatagaacc caagcagtgg aaacgataac ttggaagaaa gttgatgagg 900

aacatcttta catgactgaa catcagatag gtgctgccga aggacagatg gtagttaacg 960

aggatgagct ttctataact gaaattggaa tggggagagg tgataaaatt cagcatgtgc 1020

tttctgagga agagctttca tggtctgaag atgaagtgca gttaattgag gatgatggac 1080

aatatgaagt tgatgagacc tctgtgtccg ttaacgttga acaagatatc caggggtcac 1140

cacaggatgt tgtggatccg caagcactaa aggtgatgct gcaagaactc gctgagaaaa 1200

attattcgat gaggaacaag ctgtttgttt ttccagaggt agtgaaagct gattcagtta 1260

ttgatcttta tttcaatcgt gacctaacag ctttggcgaa tgaacccgat gttgtcatca 1320

aaggagcatt caatggttgg aaatggaggc ttttcactga aagattgcat aagagtgacc 1380

ttggaggggt ttggtggtct tgcaaactgt acatacccaa ggaggcctac agattagact 1440

ttgtgttctt caacggtcgc acggtctatg agaacaatgg caacaatgat ttctgtatag 1500

gaatagaagg cactatgaat gaagatctgt ttgaggattt cttggttaaa gaaaagcaaa 1560

gggagcttga gaaacttgcc atggaagaag ctgaaaggag gacacagact gaagaacagc 1620

ggcgaagtaa ggaagcaagg gctgcagatg aagctgtcag ggcacaagcg aaggccgaga 1680

tagagatcaa gaacaaaaaa ttgcagagta tgttgagttt ggccagaaca tgtgttgata 1740

atttgtggta catagaggct agcacagata caagcggaga tactatcagg ttatactata 1800

acagaaactc gaggccactt gcgcatagta ctgagatttg gatgcatggt ggttacaaca 1860

attggtcaga tggactctct attgttgaaa gctttgtcaa gtgcaatgac agagacggcg 1920

attggtggta tgcagatggt acgacacctc aacctttgta cataaggcaa cattgttttg 1980

atttttttg ttgaggaaac atttgttttg attctagcat aatgctccta caaatatggc 2040

atgaatttcc ttgtttttatt gatgtcatga gaaagtattt tattaactcg aaggccatgg 2100

aagctcaaca tttaccatag acagacgctt aaagatcatt tgtattccgt ggatcatata 2160

tgtaatgtaa tacctgtctt ttctctatat gtacagttat tccacctgaa aaagcacttg 2220

tgttggactg ggttttttgct gatgggccag ctgggaatgc aaggaactat gacaacaatg 2280

ctcgacaaga tttccatgct attcttccaa acaacaatgt aaccgaggaa ggcttctggg 2340

tgcaagagga gcaaaacatc tatacaaggc ttctgcaaga aaggagagaa aaggaagaaa 2400

ccatgaaaag aaaggtgagt tgcaacaaaa tctttgcata tagatc         2446
```

```
<210> 13
<211> 1032
<212> DNA
<213> Triticum sp.

<400> 13
gatctctata attttggcag ttaacccctg agtgatggca aatatattcc ctttcgtcta 60

ttttccaaat tcaaaatgca tggttccatg caagcttatc caaaatcact tgataatata 120
```

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```
ccaatcacaa cataactttg tttaccataa gaacattcct acttaaaatt tgcaaggtaa 180

ctccctttcg aggctggttg gcttgatgag taactggcaa ttaacaaaga aaagatatat 240

ctgatgtttg gaacaaaaca tatgatcagg gttgtttggg ttgactcatg ttccttttta 300

cctacacagg ctgagagaag tgcaaatatc aaagctgaga tgaaggcaaa aactatgcga 360

aggtttctgc tttcccagaa acacattgtt tataccgaac cgcttgaaat acgtgccgga 420

accacagtgg atgtgctata caatccctct aacacagtgc taaatggaaa gccggaggtt 480

tggtttagat gctcttttaa cctttggatg catccaagtg gagcattgcc accccagaag 540

atggtgaaat caggggatgg gccgctctta aaagccacag gtttattgcg ttattacatc 600

actgttatta gtatatatat aaccattttt atgcaatcaa tagagtcaag tgcaactaat 660

gatgcacaga taggatcaca tcattaggag aatgatgtga tggacaagac ccaatcctaa 720

gcatagcaca agatcgtgta gttcgttcgc tagagctttt ctaatgtcaa gtatcatttc 780

cttagaccat gagattgtgc aactcccgga tatcgtagga gtgctttggg tgtatcaaat 840

gtcacaacgt aactgggtga ctataaaggt gcactacagg tatctccgaa agtttctgtt 900

gggttggcac gaatcgagac tgggatttgt cactccgtat gacggagagg tatctttggg 960

cccactcggt aatgcatcat cataatgagc tcaatgtgac taaggagtta gccacgggat 1020

cgagaattcc cg                                                      1032
```

<210> 14
<211> 892
<212> DNA
<213> Triticum sp.

<400> 14
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aatatttctt gttctattat tggtaataat tagctagttt aatgccataa gcccataaca 60

gatatgcaac tactccctcc aatccatatt acttgtcgca actttggtac aactttagta 120

caaagttata ctaaagctgt gacaagtaat atggaccgga gggagtacta tataagcttg 180

tagctgtttt gagaccgagt gtctgctcgg gtggctagct ggagcgggct gaagtgcttg 240

caggcacctc ttctctagaa aaaagtgctt gcagccccccc cgcccccctcc atagggtgag 300

tggtcacctt tcttcttaaa aattatggca ccaagggaaa ttctcggctg gtcgagcttg 360

tagctatttt ttcggagcgt gaatgggagc gtctttctgt ataaggccta taggcttact 420

ttgatatata ttgtgaagtc acttaagcct gttaaaacg tagaaactta gttccgcaac 480

ttggccaaat ccctgttaaa ttggtttact gtgtactaga tgcatcgatg gcgcagagtc 540

ccggggggta ataaagcttc cattttctac aatgaagtta attatcctac ttgccttgta 600

attactgagt acaatacaga gcaccgaaaa gctgtatcct tcctacttcc ttatgtttat 660

ctgtgttcct tgtctagtta atgttccacc ggatgcctat atgatggact ttgtttctc 720

cgagtgggaa gaagatggga tctatgacaa caggaatggg atggactatc atattcctgt 780
```

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```
ttctgattca attgaaacag agaattacat gcgtattatc cacattgccg ttgagatggc 840

ccccgttgca aaggtaatat aattctaagg ctagtttctt tgatgcgagg cg        892


<210> 15
<211> 871
<212> DNA
<213> Triticum sp.

<400> 15
aggttatcct ccagaatgaa tttttttccag tacgtattat ttagaatact agcggtatat 60

tgactttttc tttgtgagac tacacttttct tgtttaccat tccagtgcac catgttcaaa 120

atcttgtatt cagcgcgtta ctttcagttt ctttactact agcttatttg gtgcattggt 180

gtttccttttc ctactctact atctgaatgc tacttgtgtt ttcgcaacag ttgcttctttt 240

atcccccttcc atttctcagt taaaaaaact tgcatctgta ttcacgtgac agcatataat 300

acattgccat gattggtcaa gtgctccggt cgcctggcta tataaggaac actattccca 360

atccagaatg gcaagcactc gggttgtatt taccatccac aatcttgaat ttggagcaca 420

ttatattggt aaagcaatga catactgtga taaagccaca actgtgagtg ccttactgtc 480

ttgtaatttt taatctttct gtttggcgca cagaaaatct tccacatttt acagaatcat 540

gttcttgtgt tttgtacgta ttcaactatt tccacccaaa cttttcaggt ttctcctaca 600

tattcaaggg acgtggcagg ccatggtgcc attgctcctc atcgtgagaa attctacggc 660

attctcaatg gaattgatcc agatatctgg gatcctgatt gccaacatgc tgtttggtcg 720

tctcgaggtc tttacattgc tggtgctctt tacccccgact ttctggcgtg aatgatggag 780

taatacgtga aaacattaat tcttttctca acaagggacg gacaaacgcg cgagattgcc 840

tcctacctgg cttcggaact gaaagaactg g                                871


<210> 16
<211> 1592
<212> DNA
<213> Triticum sp.

<400> 16
cgggaattct cgatcccgtg gctaactcct tagtcacatt gagctcatta tgatgatgca 60

ttaccgagtg ggcccaaaga tacctctccg tcatacggag tgacaaatcc cagtctcgat 120

tcgtgccaac ccaacagaaa ctttcggaga tacctgtagt gcacctttat agtcacccag 180

ttacgttgtg acatttgata cacccaaagc actcctacga tatccgggag ttgcacaatc 240

tcatggtcta aggaaatgat acttgacatt agaaaagctc tagcgaacga actacacgat 300

cttgtgctat gcttaggatt gggtcttgtc catcacatca ttctcctaat gatgtgatcc 360

atacactgac aattttatcc cggtaccaga tttttttccca gagtgcaagt agatatatac 420

caaggccaca gatagtttta tgcttaacta tgtgtttcat actacttcag gtcccttata 480

cttgtgagaa tgttgtcgaa ggcaagagag ctgcaaaaag ggccttgcag cagaagtttg 540
```

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```
gattacagca aactgatgtc cctattgtcg gaatcatcac ccgtctgaca gcccagaagg 600

gaatccacct catcaagcac gcaattcacc gaaccctcga aagcaacgga caggttcatc 660

atcccttgtg aacgaataaa catcaaacgt tttgtttata aaaagttgct tactatttgt 720

ttttgtttac ttcaaaacaa aagtctgaaa atgaagtgtt tggttcctag gtggttttgc 780

ttggttcagc tccagatcat cgaatacaag gcgatttttg cagattggcc gatgctcttc 840

acggtgttta ccacggtagg gtgaagcttg ttctaaccta cgatgagcct ctttctcacc 900

tggtgagctc caatatccta cacaccatct agccagccct tcattatggg agctggagac 960

tactttataa tttaggttga tgatcgatca tgctgcagat atacgctggc tccgacttca 1020

ttattgtccc ttcaatcttc gaaccctgtg gcttaacaca acttgttgcc atgcgttatg 1080

gatcgatccc tatagttcgg aaaaccggag gtgtgtgact atttctctcc attatgctgc 1140

actgatttgc atatgtcgag ctgttggaca tgaaatggaa actatccttt ggtatcgcag 1200

gactttacga cactgtcttc gacgtagaca atgataagga ccgggctcgg tctcttggtc 1260

ttgaaccaaa tgggttcagt ttcgacggag ccgacagcaa cggcgtggat tatgccctca 1320

acaggcaagt atcgttcctc aattagccct gaattcagca gtagtgctag gttatttacc 1380

ttgcatgttc catacctcat ttcagagcaa tcggcgcttg gttcgatgcc cgtgattggt 1440

tccactccct gtgtaagagg gtcatggaac aagactggtc atggaaccgg cccgcactgg 1500

actacattga attgtaccat gccgctcgaa aattctgaca cccaactgaa ccaatggcaa 1560

gaacaagcgc attgtgggat cgagaattcc cg                                 1592
```

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<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 17
Asp Val Gln Leu Val Met Leu Gly Thr Gly
  1               5              10


<210> 18
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 18
Ala Ala Gly Lys Lys Asp Ala Gly Ile Asp
  1               5              10


<210> 19
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```
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 19
Ala Thr Gly Lys Lys Asp Ala Gly Ile Asp
 1               5               10


<210> 20
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 20
Ala Leu Gly Lys Lys Asp Ala Gly Ile Asp
 1               5               10


<210> 21
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 21
Ala Thr Gly Lys Lys Asp Ala Leu
 1               5


<210> 22
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 22
Ala Leu Gly Lys Lys Asp Ala Leu
 1               5


<210> 23
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 23
Ala Ala Gly Lys Lys Asp Ala Arg Val Asp Asp Asp Ala Ala
 1            5                  10
```

```
<210> 24
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 24
Ala Leu Gly Lys Lys Asp Ala Gly Ile Val Asp Gly Ala
 1               5                  10


<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 25
tgttgaggtt ccatggcacg ttc                          23


<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 26
agtcgttctg ccgtatgatg tcg                          23


<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 27
ccaagtacca gtggtgaacg c                            21


<210> 28
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 28
cggtgggatc caacggccc                               19


<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:PRIMER

<400> 29
ggaggtcttg gtgatgttgt                                              20


<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 30
cttgaccaat catggcaatg                                             20


<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 31
cattgccatg attggtcaag                                             20


<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 32
accacctgtc cgttccgttg c                                           21


<210> 33
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 33
gcacggtcta tgagaacaat ggc                                         23


<210> 34
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 34
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tctgcatacc accaatcgcc g                                      21


<210> 35
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 35
Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Val
  1               5                  10                  15

Gln Asp Leu Gly His Asn Val Glu Val
            20                  25


<210> 36
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PEPTIDE MOTIF

<400> 36
Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Ile
  1               5                  10                  15

Gln Asp Leu Gly His Thr Val Glu Val
            20                  25



<210> 37
<211> 9024
<212> DNA
<213> Triticum sp.

<400> 37
aaatatgaaa ccaaaaaaaa aatagaaaaa ggaaaggtaa aatagaaagt taaataggaa 60

taatggataa aaaataaaac atcaaagaaa aacgaaatgc agaagaaaaa aacgtcactt 120

gttcccttat tatctcccgt gcaccccggt agcgtaggac aaaaagaaaa aatagaacgg 180

acccaacgtc acaagctcac acatgcccag cgagagaaaa gaaaaatggt gcgacaaaaa 240

aaaggaaacg ggctgagagc cgaaacacat gggctgcgct ttgttcgcta cgaagctctc 300

ccctcgacaa aatatgaatc gcgacgtgat tggatcctat ggtggaaaaa gtgaatgaga 360

ccaaaagaat tctcagctga atgagtttta gcaagactga tcattatatc caacataaat 420

agattttttt tttgcaaaaa taatccaaat ctattagcaa agttcagtag aagtacaaag 480

catctcgaac attataaaca ttacactgag attccaggac caccaaacaa cccactactg 540

ccgcgaaaag aaaaggattc ggaagacaga aattatccaa accacgttcg tccttggttg 600

ttggtctcat tgcgcgctaa acaacctgga cagcagaaga agcaaagcag tgtgcttccg 660

ctccgcagca agaagacaag tcgtcacatg tcagacgccg tcactcaagc aagcaaactg 720

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caatgcttct cgttcggttt atcccctagc acgcacgaac gcatgtgccg caccgcgtca 780

cgcaacgcat gcatgcacaa accaacaaac gaaacagtgc agttgcagtg ctctatctac 840

atatacgcaa tcaacgcggg cctcctcctt cgccgcgagc cccgttccgt cctcggtctt 900

cacgtggatt ttgcaacttc cttccagcag cttgtcacca cggacgcttc ctctctgaca 960

actggccccg tgggcggaac ggggcctccg ctcgcccctt gcgaaaccca cggctcgtcc 1020

gttcgcttct ctagcgggca ccgacagaag gggccggcgc agggtaggac caggctgtca 1080

gctggtgagg agcctgccgc tcgttgtgcc gcagctggag accgagcggg gcaacggaac 1140

ggctgccgcc ctcgtgtgct gctcgcgtgg cacgccgcaa cggcaccggg cccgctttcc 1200

agcgtgctcg cccgcaaacc gcagacccaa cacgccagcc gccaggggggc cgttcgtacg 1260

tacccgcccc tcgtgtaaag ccgccgccgt cgtcgccgtc ccccgctcgc ggccatttct 1320

tcggcctgac cccgttcgtt tacccccaca cagagcacac tccagtccag tccagcccac 1380

tgccaccgcg ctactctcca ctcccactgc caccacctcc gcctgcgccg cgctctgggc 1440

ggaccaaccc gcgaaccgta ccatctcccg ccccgatcca tgtcgtcggc ggtcgcgtcc 1500

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# PATENT COOPERATION TREATY

## PCT

**INTERNATIONAL PRELIMINARY EXAMINATION REPORT**

(PCT Article 36 and Rule 70)

| Applicant's or agent's file reference 2288545/MRO/wm | **FOR FURTHER ACTION** | See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416). |
|---|---|---|

| International Application No. **PCT/AU00/00385** | International Filing Date *(day/month/year)* 28 April 2000 | Priority Date *(day/month/year)* 29 April 1999 |
|---|---|---|

International Patent Classification (IPC) or national classification and IPC

**Int. Cl.** [7]   C12N 15/54; A01H 1/00, 5/00; C08B 3/02; C12N 9/10, 15/11; C12Q 1/48, 1/68

Applicant

COMMONWEALTH SCIENTIFIC & INDUSTRIAL RESEARCH ORGANISATION *et al*

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1.      This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.

2.      This REPORT consists of a total of   4   sheets, including this cover sheet.

[ ]     This report is also accompanied by ANNEXES, i.e., sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

These annexes consist of a total of     sheet(s).

3. This report contains indications relating to the following items:

| | | |
|---|---|---|
| I | [X] | Basis of the report |
| II | [ ] | Priority |
| III | [ ] | Non-establishment of opinion with regard to novelty, inventive step and industrial applicability |
| IV | [ ] | Lack of unity of invention |
| V | [X] | Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement |
| VI | [X] | Certain documents cited |
| VII | [ ] | Certain defects in the international application |
| VIII | [ ] | Certain observations on the international application |

| Date of submission of the demand 31 October 2000 | Date of completion of the report 30 March 2001 |
|---|---|
| Name and mailing address of the IPEA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustralia.gov.au Facsimile No. (02) 6285 3929 | Authorized Officer **GARETH COOK** Telephone No. (02) 6283 2541 |

Form PCT/IPEA/409 (Cover sheet) (July 1998)

| I. | Basis of the report |
|----|----|

1. With regard to the **elements of the international application:**\*

    [X] the international application as originally filed.

    [ ] the description,    pages  ,  as originally filed,

                              pages  ,  filed with the demand,

                              pages  ,  received on  with the letter of

    [ ] the claims,    pages  ,  as originally filed,

                              pages  ,  as amended (together with any statement) under Article 19,

                              pages  ,  filed with the demand,

                              pages  ,  received on  with the letter of

    [ ] the drawings,    pages  ,  as originally filed,

                              pages  ,  filed with the demand,

                              pages  ,  received on  with the letter of

    [ ] the sequence listing part of the description:

                              pages  ,  as originally filed

                              pages  ,  filed with the demand

                              pages  ,  received on  with the letter of

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.
These elements were available or furnished to this Authority in the following language  which is:

    [ ] the language of a translation furnished for the purposes of international search (under Rule 23.1(b)).

    [ ] the language of publication of the international application (under Rule 48.3(b)).

    [ ] the language of the translation furnished for the purposes of international preliminary examination (under Rules 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, was on the basis of the sequence listing:

    [X] contained in the international application in written form.

    [X] filed together with the international application in computer readable form.

    [ ] furnished subsequently to this Authority in written form.

    [ ] furnished subsequently to this Authority in computer readable form.

    [ ] The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

    [ ] The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished

4. [ ] The amendments have resulted in the cancellation of:

    [ ] the description,    pages

    [ ] the claims,    Nos.

    [ ] the drawings,    sheets/fig.

5. [ ] This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed, as indicated in the Supplemental Box (Rule 70.2(c)).\*\*

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\*    *Replacement sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to this report since they do not contain amendments (Rules 70.16 and 70.17).*

\*\*    *Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report*

| V. | Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement |
|----|----|

| 1. | Statement | | |
|----|----|----|----|
| | Novelty (N) | Claims **9, 20, 39 and 40** | **YES** |
| | | Claims **1-8, 10-19, 21-38 and 41-59** | **NO** |
| | Inventive step (IS) | Claims **9, 20, 39 and 40** | **YES** |
| | | Claims **1-8, 10-19, 21-38 and 41-59** | **NO** |
| | Industrial applicability (IA) | Claims **1-59** | **YES** |
| | | Claims | **NO** |

**2.** Citations and explanations (Rule 70.7)

The following documents identified in the International Search Report have been considered for the purposes of this report:

D3 WO 97/45545 (HOECHST SCHERING AGREVO GmbH)
D4 Walter L *et al*, (a) GenPept Accession AAB17085 and (b) GenBank accession U66377
D5 Gao M *et al*, GenPept accession AAC14014
D6 GenPept accession AAC14015
D7 D'Hulst C *et al*, GenPept accession AAC17969
D8 Bullar SS *et al*, GenPept accession CAB40374

<u>Novelty (N) and Inventive Step (IS) claims 1-8, 10-19, 21-38 and 41-59</u>
Document D3 discloses sequences (SEQ ID NO: 5) which fall within the condition of 85% identity to SEQ ID NO's 1-6, 50 and 53. The document also teaches using these sequences which encode starch synthase, to transform plants. As such the invention as defined in claims 1-8, 10-19, 21-38 and 41-59 is not novel and lacks an inventive step under Article 33 of the PCT.

Documents D4(a) GenPept acc. no AAB17085 and D4(b) GenBank acc. no.U66377 disclose a peptide sequence for the wheat starch synthase and its encoding nucleotide sequence. These sequences falls within the criterion of 85% identity to the sequences defined in claims 1 and 12. As such the invention as defined in claims 1-8, 10-19 and 21 is not novel and lacks an inventive step under Article 33 of the PCT.

It would be obvious for a PSA to combine the information on the sequences in D4(a) or (b) with the teaching on the transformation of plants in D3 to transform plant using these sequences. As such the invention as defined in claims 21-38 and 41-59 lacks an inventive step under Article 33 of the PCT in the light of the combined teaching of D3 and D4.

Documents D5-D8 discloses sequences which contain the sequence defined in claim 18 (a)-(h): D5 discloses (a), (c) and (d); D6 discloses (c), (d) and (e); D7 discloses (f), and; D8 discloses (b). As such the invention as defined in claim 18 lacks novelty and does not involved an inventive step under Article 33 of the PCT.

<u>Industrial applicability:</u>
The invention as defined in claims 1-59 is useful in agriculture and food production, as such it has industrial applicability.

| VI. | **Certain documents cited** |
|---|---|

| 1. | Certain published documents (Rule 70.10) |
|---|---|

| Application No. Patent No. | Publication date *(day/month/year)* | Filing date *(day/month/year)* | Priority date ( valid claim) *(day/month/year)* |
|---|---|---|---|

The inventors of the present application authored document D1 (Li Z *et al*, Plant Physiology, August 1999, 120(4):1147-1156) disclosing the same subject matter as the current application.

Documents D2(a) and D2(b) (Gao M *et al*, GenPept accession CAB86618 and GenBank accession AJ269502) disclose sequences which fall within the criterion of 85% identity to SEQ ID NO's 1-6, 50 and 53 of this application.

These documents are published after the priority date of the present application.

| 2. | Non-written disclosures (Rule 70.9) |
|---|---|

| Kind of non-written disclosure | Date of non-written disclosure *(day/month/year)* | Date of written disclosure referring to non-written disclosure *(day/month/year)* |
|---|---|---|

| A. | CLASSIFICATION OF SUBJECT MATTER |
|---|---|

Int. Cl. [7]:   C12N 15/54, 15/11; C12N 9/10; C12Q 1/48, 1/68; A01H 1/00, 5/00; C08B 3/02.

According to International Patent Classification (IPC) or to both national classification and IPC

| B. | FIELDS SEARCHED |
|---|---|

Minimum documentation searched (classification system followed by classification symbols)
WORLD PATENT INDEX (WPI).

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
GENBANK, EMBL, SWISS-PROTEINS, PIR

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
KW: WPI Starch synthase. Seq id nos 2, 4, 6, 8, 10 and 39-54.

| C. | DOCUMENTS CONSIDERED TO BE RELEVANT | |
|---|---|---|
| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| P, X | Li Z *et al* "The localization and expression of the class II starch synthases of wheat" Plant Physiol 1999 Aug 120(4) pp 1147-1156. See the whole document. | 1-59. |
| P, X | GenPept accession no. CAB86618, and GenBank accession no. AJ269502, published 7 April 2000. Gao M and Chibbar R N "Isolation, characterization and expression analysis of starch synthase IIa c DNA from wheat (Triticum aestivum L.)" See the whole document. | 1-8, 10-19 and 21 (seq id nos 1-6, 50 and 53) |
| X;<br>Y | WO 97/45545 A (HOECHST SCHERING AGREVO GmbH) 4 December 1997. See the whole document especially the examples and seq id no 5. | 1-8, 10-19, 21-38 and 41-59 (seq id nos 1-6, 50 and 53) |

| [X] Further documents are listed in the continuation of Box C | [X] See patent family annex |
|---|---|

| * | Special categories of cited documents: | "T" | later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
|---|---|---|---|
| "A" | document defining the general state of the art which is not considered to be of particular relevance | | |
| "E" | earlier application or patent but published on or after the international filing date | "X" | document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone |
| "L" | document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | ."Y" | document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| "O" | document referring to an oral disclosure, use, exhibition or other means . | | |
| "P" | document published prior to the international filing date but later than the priority date claimed | "&" | document member of the same patent family |

| Date of the actual completion of the international search<br><br>16 June 2000 | Date of mailing of the international search report<br><br>2 0 JUN 2000 |
|---|---|
| Name and mailing address of the ISA/AU<br><br>AUSTRALIAN PATENT OFFICE<br>PO BOX 200, WODEN ACT 2606, AUSTRALIA<br>E-mail address: pct@ipaustralia.gov.au<br>Facsimile No. (02) 6285 3929 | Authorized officer<br><br><br>J.H. CHAN<br>Telephone No : (02) 6283 2340 |

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

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END OF ANNEX